AMINO ACID SEQUENCES OF A CONSERVED PORTION OF Tbp1 PROTEIN FOR CONSTRUCTION OF DEGENERATE PRIMERS USED IN PCR AMPLIFICATION OF A PORTION OF THE M. cattarhalis 4223 tbpA GENE.

NEVTGLG

SEQ ID NO: 17

GAINEIE

SEQ ID NO: 18

FIG.1

BEST AVAILABLE COPY

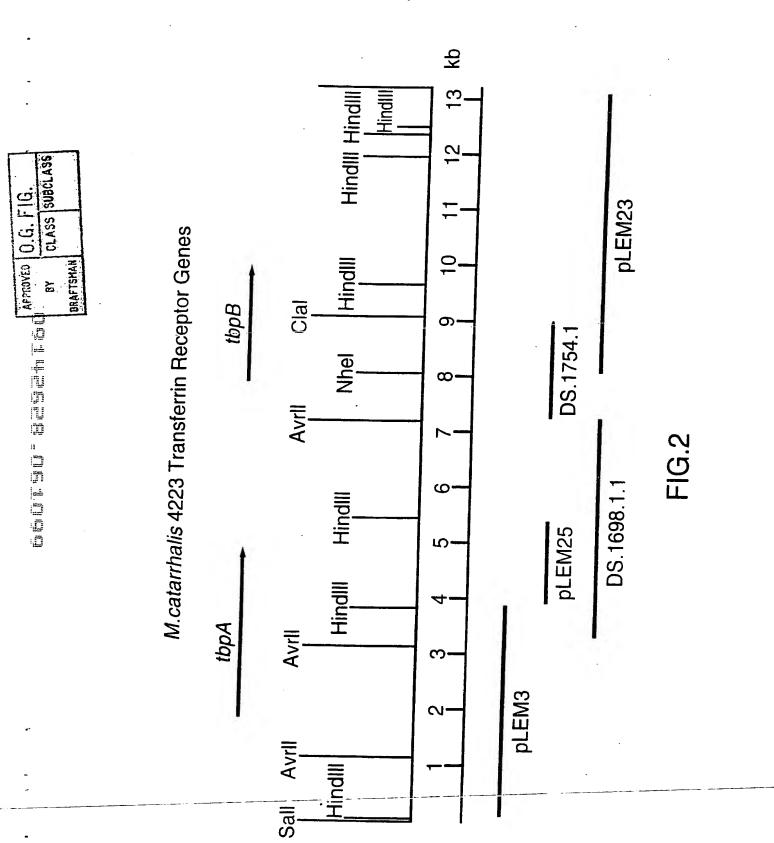
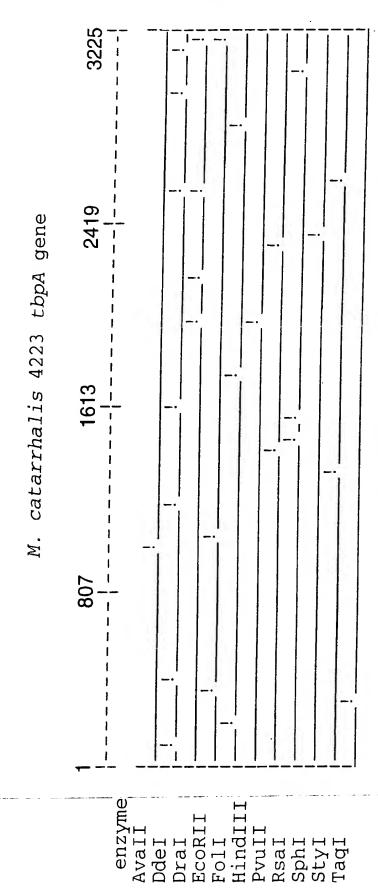
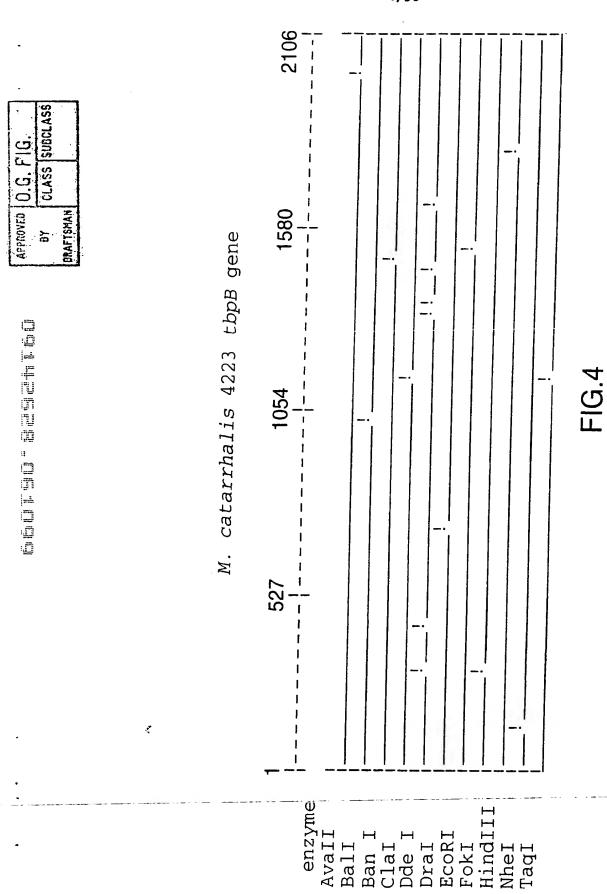


FIG.3

BRAFTSMAN



Pvull Rsal Sphl Styl Tagl



SUBSTITUTE SHEET (RULE 26)

216 **ACA** Thr

GTT Val

GAA Glu

GCC AAC Ala Asn

AAA (Lys)

CGT

Ala

CCC

189 AAA Lys

AAG Lys

GCG Ala

ACA Thr

ACT GTT GTA Thr Val Val

GAA Glu

 \mathtt{GAT}

AAC

	100	
F1G.	SUBCLASS	
0.G. F	CLASS	
APPROVED	≯ 60	BRAFTSHAH

Sequence of M. catarrhalis 4223 tbpA gene

TTGATG¢CTGCCTTGTGATTGGTTGGGTGTATCGGTGTATCAAAGTGCAAAAGCCAACAGGTGGTCATTG TATTTTGGTAAACAATTAAGTTCTTAAAAACGATACACGCTCATAAACAGATGGTTTTTGGCATCTGCAAT

54	AAA Lys	108 AAC Asn	162 TTG Leu
	TTA	GCA Ala	GTC Val
	GTA Val	CTG Leu	GTT Val
	CAA Gln	GCA Ala	GTT GTT GTC Val Val Val
,	AAA Lys	GTG Val	CTT Leu
((Ser	CAG Gln	AAC Asn
6	MET Asn Gln Ser Lys Gln Asn Asn Lys Ser Lys Lys Ser Lys Gln Val Leu Lys	81 CTT AAC ATC ACG CAG GTG GCA CTG GCA AAC Leu Asn Ile Thr Gln Val Ala Leu Ala Asn	ACG GCC GAT AAG GCG GAG GCA ACA GAT AAG ACA AAC CTT G Thr Ala Asp Lys Ala Glu Ala Thr Asp Lys Thr Asn Leu V
ج د د	AAA Lys	ATC Ile	AAG Lys
Ç	Ser	AAC Asn	GAT Asp
27	Lys	81 CTT Leu	135 ACA Thr
ر د د	Asn	CTG	GCA Ala
ر د د	Asn	GGT	GAG Glu
۵ م	Gln	TTG GGT CTG	GCG Ala
AAA	Lys	TCT Ser	AAG Lys
TCA	Ser	TTG Leu	GAT Asp
CAA	Gln	<u>GCC</u> Ala	GCC Ala
AAT	Asn	CTT AGT GCC Leu Ser Ala	ACG
ATG	MET	CTT	ACA Thr
A.	2;	ОIП	K E

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		270 CTA Leu	324 GGT Gly	378 GCG Ala	432 GTG Val	486 AAT Asn	540 GGG Gly
O.G. FIG.		GTG Val	CAA Gln	GTG Val	ccr Pro	GAA Glu	TCT
O.G. F		CAA Gln	GAG Glu	cgt Arg	$oldsymbol{GGC}$	TAC Tyr	GGC Gly
APPROVED O.G. FIG. BY CLASS SUBG		GAA Glu	GTT Val	AAT Asn	CAA Gln	GAA Glu	TAC
<u> </u>		AAA Lys	GīG Val	AAA Lys	CTA Leu	ATA Ile	GAA Glu
, 1750 1750 1750		AAT Asn	GCT Ala	gat Asp	GCC Ala	GAA Glu	AGT Ser
ū		ATC Ile	ATT Ile	ATG MET	tat Tyr	AAC Asn	TCA Ser
		ACC Thr	$\frac{GGC}{G1Y}$	GRT ${\tt GGT}$	CAC His	ATC Ile	AAT Asn
		GAG Glu	ccr Pro	cgt Arg	cag Gln	GCA Ala	GCA Ala
		243 GCC Ala	297 GAC Asp	351 ATT Ile	405 GCC Ala	459 GGG Gly	513 GGT G1y
		ACT Thr	tat Tyr	rcr Ser	CAA Gln	$\textbf{GGT}\\ \text{G1} \text{Y}$	AAA Lys
		AAA Lys	CGC Arg	tat Tyr	AAT Asn	GCA Ala	AGT Ser
		GTC Val	ACA Thr	GGC G1y	ATC Ile	GCC Ala	GAG ATT Glu Ile
		GTG Val	TTA Leu	TCA Ser	$ extstyle{GGC}{G1}$	tat Tyr	GAG Glu
•		AAG Lys	gac Asp	AGC Ser	gat Asp	AAT Asn	GTT Val
•		$\texttt{GGT}\\ \texttt{G1}\underline{\mathtt{y}}$	cga Arg	GCA Ala	GTT Val	AAA Lys	TCC
	FIG.5B	CTT Leu	ATT Ile	GGG G1y	TTG Leu	GGC G1y	CGC Arg
	FIG	${\tt GGG}\atop{\tt Gly}$	AAC Asn	cgt Arg	GTA Val	GCA Ala	GTC Val

918 AAT Asn

GTC Val

AAG Lys

GAT Asp

CGT Arg

GTG Val

AAT Asn

ACC Thr

CCA Pro

891 AAG Lys

GCC

CTT Leu

AAA Lys

ACC

CAA Gln

GGT Gly

GGC

-	594	648	702	756	810	864
	AAA	AAC	CTT	TAT	CGA	GCT
	Lys	Asn	Leu	TY <i>r</i>	Arg	Ala
SCLASS	ATC	AAT	GGT	GCC	AAC	GCT
	Ile	Asn	Gly	Ala	Asn	Ala
O.G. F1G.	ATC	AAA	AGC	GAT	AAT	TGT
class subclass	Ile	Lys	Ser	Asp	Asn	Cys
	GAC	AGT	TTT	GAT	CCA	GCG
	Asp	Ser	Phe	Asp	Pro	Ala
APPROVED BY DRAFTSHAN	GAT Asp	GCC Ala	TCT	CAT His	GAC Asp	GAG Glu
	GCC Ala	\mathtt{TAT}	GGT Gly	GCA Ala	ACT Thr	TAT Tyr
	ACC	GCC	GCA	AAG	ACC	AAT
	Thr	Ala	Ala	Lys	Thr	Asn
	AAA Lys	ACC Thr	AAG Lys	\mathtt{TAC}	GCA Ala	$_{\rm GGT}$
	ACC	AAA	GGC	GAA	GTG	AAT
	Thr	Lys	Gly	Glu	Val	Asn
	567	621	675	729	783	837
	GTT	ACC	GCA	CAA	GCG	GCC
	Val	Thr	Ala	Gln	Ala	Ala
	TTT	CAG	GCA	GGT	AGA	TGT
	Phe	Gln	Ala	Gly	Arg	Cys
****	GCA	GTG	GCA	CGT	GAT	GAA
	Ala	Val	Ala	Arg	Asp	Glu
	GTG	GGC	GTG	CGC	TTT	AAT
	Val	Gly	Val	Arg	Phe	Asn
	TCT	TGG	TCT	GAC	AGT	GCA
	Ser	Trp	Ser	Asp	Ser	Ala
•	GGC Gly	GAT Asp	AAT Asn	ACC Thr	CAA	ATA Ile
•	TCT Ser	AAA Lys	GTT Val	TAC Tyr	AGC	TTA ATA GCA Leu Ile Ala
FIG.5¢	GCA TTA Ala Leu	GG <u>T</u> G1⅓	TGG	ATC Ile	GGT Gly	TTT Phe
FIG.	GCA	GAT	GCA Ala	ATC Ile	CAG Gln	ACA Thr

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[w]		972 CAA GAC Gln Asp	1026 TAT GTC Tyr Val	1080 ACC GTG Thr Val	1134 CAT GCC His Ala	1188 GAT ACC ASP Thr	1242 TAT GAT Tyr Asp
G. SUBCLASS		ACC Thr	CAC His	AAA Lys	AAC Asn	CGT Arg	TTT Phe
0.G. FIG.		CTC Leu	AAG Lys	GAT Asp	AGC Ser	ATT Ile	GTA Val
APPROVED 67 BRAFTSMAN	*	CCA Pro	GAT Asp	CAA Gln	CTC Leu	CGC Arg	GGC Gly
	÷	AAC Asn	AAC Asn	ATG MET	AGG Arg	GAA Glu	CAT
3 때 때 때 때 때 1. 다 []		CCA Pro	CTA Leu	GCC Ala	TCA Ser	GGT Gly	GCT Ala
T T		ATC Ile	CAG	\mathtt{TAC}	AAA Lys	CTT Leu	TAT Tyr
fi		CTT Leu	\mathtt{TAT}	AAC Asn	GAA Glu	AAT Asn	AAC Asn
		945 CGC Arg	999 GGT GlY	1053 . CAA . Gln	1107 ATT Ile	1161 AAT Asn	1215 ATC . Ile
		AAC Asn	CCA Pro	1 AAA Lys	1 GAC Asp	1 GGC Gly	1 GGC Gly
		CCT	CGC Arg	ACC Thr	CAT His	CAA Gln	\mathtt{TAT}
		${\tt GGT} \\ {\tt G1} \\ {\tt Y}$	CTT Leu	ATC Ile	GTT Val	${\tt TAT} \\ {\tt TY} {\tt Y} {\tt Y}$	$_{\rm G1y}^{\rm GGT}$
		ACA Thr	CTG	GAA Glu	ACG Thr	\mathtt{TAT}	TCA Ser
		TAT Tyr	TTA Leu	\mathtt{TAT}	CTG Leu	GGC Gly	GAT Asp
•		GAT Asp	TCC Ser		TAT Tyr	AAT Asn	CCA GAT Pro Asp
• • • • • • • • • • • • • • • • • • • •	.50	AAA Lys	AAA Lys	GGT GTG Gly Val	GCT Ala	GCC	666 G1y
	FIG.5D	GTC Val	AGC Ser	GGT Gly	CCT Pro	CAA Gln	ATT Ile

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-		1296 AAA GGT Lys Gly	1350 ACG Thr	1404 GAC AAA ASP LYS	1458 AAC AAT Asn Asn	1512 ATG GCG MET Ala	1566 2 AAT 3 ASD	1620 CAA AAA Gln Lys
ASS		AAA Lys	ATT Ile	1 GAC Asp	1 AAC Asn	1 ATG MET	1 TTC Phe	
O.G. FIG.	_	AGC Ser	GAC Asp	ATT Ile	GAT Asp	AAA Lys	AAA Lys	TAT Tyr
APPROVED 0.G. FIG.	AM	GAC Asp	CAA Gln	CAC	GTG Val	AAA Lys	GAT Asp	TCT Ser
APPROV	BRAFTSMAIL	ТАТ Ту <i>т</i>	AAG Lys	CCG	GAG Glu	AAC Asn	$\mathtt{TAT}\\ \mathtt{TYr}$	CAG Gln
		GTT Val	GAT Asp	$\mathtt{TAT}\\ \mathtt{TY} r$	AAA Lys	TTT Phe	GGC Gly	CAT His
<u>.</u>		\mathtt{TAT}	\mathtt{TAT}	ACC Thr	GTA Val	GTC Val	GTT Val	ACC
		GAA Glu	TCT Ser	TCA Ser	TCG Ser	GCC Ala	CAA Gln	GCA Ala
		CTT	GTG Val	TGT Cys	TTT Phe	AAA Lys	CTG	TTG
		1269 GGG G1y	323 CGT Arg	1377 CAC His	1431 AAA CCT Lys Pro	1485 TTA ATC Leu Ile	1539 AAC Asn	1593 CGT Arg
		1 CTA Leu	1 GTG Val	1 ACG Thr	1 AAA Lys	TTA Leu	1 ATC Ile	TAT Tyr
ii u		CGC Arg	GAT Asp	AAC Asn	AAT Asn	AAT Asn	CAC His	GAT Asp
		GAC Asp	GAT Asp	ACC Thr	GTC Val	CAC His	CAT His	GAA Glu
		AAA Lys	TTT Phe	CTG Leu	GAT Asp	CAG Gln	CAT His	CGT Arg
		CAA Gln	TGG Trp	CAG	CCT Pro	AAA GAA Lys Glu	ACG Thr	AGC
		CAC His	AAA Lys	AGC Ser	ACG Thr	AAA Lys	AGT Ser	CTG AGC
<u></u> <u>_</u>	ਜ	AAA Lys	AA'T Asn	CGC	TGT	TAC	GGC G1Y	TCA AGC Ser Ser
·	FIG.5F	GAA Glu	GAA Glu	CTA Leu	AAT Asn	GCC ' Ala'	TTG	TCA

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		1674 ATT TTA Ile Leu	1728 C CAT O His	1782 AAA AAA Lys Lys	1836 CAA GCC Gln Ala	1890 CAG	1944 CTT GGC Leu Gly
a. BCLAS		ATT Ile	1 GAC Asp	1 AAA Lys	1 CAA Gln	1 TTT Phe	CTT
O.G. FIG.		CCC	CAT His	ATC Ile	TAT Tyr	CCC	GAA Glu
APFROYED O.G. FIG		AAG Lys	$_{\rm GGT}$	GCC Ala	GAT Asp	AAA Lys	GAC Asp
BRAF		TTT Phe	\mathtt{TAT}	TTT Phe	ATT Ile	CTA Leu	ATA Ile
(***)		AAG Lys	$_{\rm GGT}$	AAT Asn	AAG Lys	ACC Thr	AAG Lys
		GAT Asp	\mathtt{TAT}	CAA Gln	GAT Asp	AGC Ser	AAC Asn
The state of the s		CCA Pro	GCT Ala	\mathtt{TAT}	ACC Thr	AAC Asn	TAC Tyr
		TTG Leu	GAT Asp	ACT Thr	AAT Asn	CCC Pro	AAA Lys
		1647 CCT Pro	1701 CTT Leu	1755 AGC Ser	1809 ACC Thr	1863 . AAC . Asn	1917 CAA GAA Gln Glu
		AAC Asn	1 TGC Cys	AAC Asn	AAA Lys	CAA Gln	1917 CAA GAA Gln Glu
		CCA CCA AGT Pro Pro Ser	ATT Ile	GCC AAA Ala Lys	CAA Gln	AAA Lys	. GGG .
		CCA Pro	CCC Pro	GCC Ala	AAC Asn	GAT Asp	TTG
		CCA Pro	AAA Lys	AAC Asn	TAC	TAT Tyr	AGT Ser
•		ACC Thr	AAC AAC Asn Asn	TGT Cys	CAA Gln	CAA Gln	CAA Gln
		TAC Tyr	AAC Asn	GCT Ala	GAG Glu	GAC	AAA Lys
	2F	GAT	TCA	CAG Gln	ATA Ile	ATT Ile	ATC AAA CAA AGT Ile Lys Gln Ser
	FIG.5F	CTT	GGT G1y	CCA Pro	GGC G1y	ATC Ile	AAA Lys

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1999	2052	2106	2160	2214	2268
AA(GCA	GAT	. GAC	AGA	CTG
AS)	Ala	Asp	Asp	Arg	Leu
1998	2052	2106	2160	2214	2268
GAC AAC	CAA GCA	GCT GAT	AAA GAC	GAC AGA	CAG CTG
Asp Asn	Gln Ala	Ala Asp	Lys Asp	Asp Arg	Gln Leu
AAT	AAT	TAT	TTA	TAT	AAC
Asn	Asn	Tyr	Leu		Asn
ACT 7	CCA / Pro /	AGC 7		CGC 1 Arg 1	AGC A
		S, S,	GCT		A(Se
TGG	CAG	AAC	ATC	GCT	GCC
Trp	Gln	Asn	Ile	Ala	Ala
GGT G	TAT Tyr	ACC AAC Thr Asn	TTC ATC Phe Ile	$_{\rm GGT}^{\rm GGT}$	AGT Ser
GCG Ala	ATC	GAG Glu	\mathtt{TAT}	CTG Leu	AAC Asn
TGG	AAT	AGC	AAT	${\tt GGG} \\ {\tt G1y}$	GTA GAC
Trp	Asn	Ser	Asn		Val Asp
GAA Glu	GAT Asp	\mathtt{TAT}	GAT Asp	TTG	GTA Val
1971	2025	2079	2133	2187	241
CGC AAC	GGC ACG	TGT AAA	GGT	GAT	TTG
Arg Asn	Gly Thr	Cys Lys	G1y	ASP	Leu
CGC		TGT	2133 AGT GGT Ser Gly	2187 GTT GAT Val Asp	2241 CCT TTG Pro Leu
TTA	AAA	AAA	ATC	\mathtt{TAT}	GTG
Leu	Lys	Lys	Ile		Val
GAT	GCC AAT	GAC	CAC	AAA	GAT
Asp	Ala Asn	Asp	His	Lys	Asp
AAA GAT Lys Asp	GCC Ala	GAT GAC Asp Asp	CGC Arg	AAT Asn	TCT Ser
AAT	AAT	AAA	ACT	ATC	AAA
Tyr	Asn	Lys	Thr	Ile	Lys
GCT Ala	CAA AAT Gln Asn	GTC	ACC ACT Thr Thr	ACC ATC A Thr Ile A	CAC
AAA	CAA	GTG	ICA	ATG ,	AAA
Lys	Glh	Val	Ser		Lys
TTT ?	AGC (ACT (Thr 1	TGC TCA	AAC A	ATC A
Phe]	Ser (Cys Ser	Asn M	Ile I

ASE	ľ	2322 TAT TYr	2376 CGC Arg	2430 TAC Tyr	2484 - AAC Asn	2538 AGT TAT Ser Tyr	2592 ACC Thr	2646 TTT Phe
O.G. FIG.		GCT Ala	GAA Glu	Z TAT TYr	TTT Phe	AGT	AGA Arg	GGC Gly
		ATC Ile	GGC G1y	CTT Leu	TCC Ser	GTT Val	ATT Ile	TTG Leu
APPROVED BY BRAFISHAH		GAC Asp	TAT Tyr	$\texttt{GGT}\\ \texttt{G1}_{\boldsymbol{Y}}$	AAA Lys	GAG Glu	GAG Glu	GAT Asp
		CTG Leu	ATG MET	AAG Lys	GAA Glu	CTT Leu	GAA Glu	
, manage		TGG Trp	GAA Glu	TGT Cys	CCT	AGT Ser	AGT Ser	AAA GGT Lys Gly
		AAT Asn	TCT Ser	GGC Gly	AAA Lys	GGC Gly	AAA Lys	GGT
5 <u>c. "d c. "h 1. C. (.)</u>		ACC Thr	TTT Phe	CAT His	CTA Leu	TTA Leu	$_{\rm GGT}$	CGT Arg
		CCC Pro	AGT Ser	CAA Gln	AAG Lys	CAC His	GTT Val	CAG Gln
		2295 AAG Lys	2349 CCA Pro	2403 ACG Thr	457 ACC Thr	511 AAC Asn	2565 ATT Ile	
		GTC Val	ATG MET	GGC G1y	2457 CAA ACC Gln Thr	2 CAT His	2 TTG Leu	2619 GGC AAA Gly Lys
		GTC Val	CGC Arg	AAA Lys	CAT His	TTA Leu	ACC GAT Thr Asp	GCA Ala
		GTG Val	TTT Phe	$_{\rm GGT}$	GTC Val	ACT Thr	ACC	AAT Asn
		GGC Gly	GGC G1y	ATC Ile	ACT Thr	GCG Ala	$\mathtt{TAT}\\\mathtt{T}\mathbf{y}\mathbf{r}$	GAT Asp
•		TTT Phe	CAA Gln	ACC Thr	CAG Gln	GGA Gly	CGC Arg	GGT
		AAT Asn	TCG Ser	GTA Val	CAG Gln	ATC Ile	AAT Asn	CAA Gln
-	5H	ניז ().	AGC	GGC Gly	TGT Cys	GAA Glu	AAA Lys	ACC (Thr (
	FIG.5H	TCT Ser	AGA Arg	TTT Phe	ATT Ile	CAA (TTT Phe	CTA Z

			·				
		2700 AGA CTT GAC Arg Leu Asp	2754 GCT TAT Ala Tyr	2808 AAC Asn	2862 ' GAT ' Asp	2916 GCC AAA Ala Lys	2970 GGC AAC ATT CAA ACA Gly Asn Ile Gln Thr
CLASS		CTT	GCT	2 ACA Thr	2 TAT Tyr	GCC	CAA Gln
O.G. FIG.		AGA	CTG	GGA Gly	GGC Gly	GAT Asp	ATT Ile
		GGC Gly	ACA Thr	GCA Ala	CTT Leu	TCT Ser	AAC Asn
APPROVED BY BRAFTSHAN		CTT Leu	TCA Ser	TTG	${\tt GGG} \\ {\tt G1} \underline{{\tt Y}}$	CAT His	GGC Gly
; === 3,		ATT Ile	TAC Tyr	ACT Thr	GTG Val	ACC Thr	AAT Asn
		AAC Asn	TTA Leu	CCA Pro	GTG Val	TTT Phe	GGT Gly
		ATT Ile	GGA Gly	AAC Asn	TAT	ATA Ile	TTA Leu
		GGC Gly	$\mathtt{TAT}\\\mathtt{TY} \mathtt{r}$	TTA Leu	CGT Arg	GCC Ala	AAC Asn
		2673 ACA Thr	2727 CCC Pro	2781 ACC Thr	2835 TCT Ser	2889 AAC Asn	2943 AAG Lys
		2 TTG Leu	CTT	2 AAA Lys	2 CCA Pro	2 GCA Ala	GAT Asp
		GAT Asp	CGC Arg	GGA Gly	CAG Gln	GGA Gly	GCA Ala
		GCT Ala	AGT Ser	AAA Lys	ATC Ile	TGG Trp	TTG Leu
		GAT Asp	AAT Asn	GTT Val	GCC Ala	AAA Lys	CTT Leu
•		CAA Gln	GTC Val	GAT Asp	GAT Asp	CAA Gln	GAG Glu
•		GGA Gly	GCT	GTT Val	TTT Phe	AGC	AGC
•	.5	AAT Asn	AAC Asn	AAA Lys	CTG	CCA AGC Pro Ser	CCA AGC Pro Ser
	FIG.51	CAT His	CTA Leu	AAC Asn	ATA Ile	GCC Ala	AAT Asn

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O.G. FIG.		3024 TCA GGT Ser Gly	3078 GTA TTT Val Phe	3132 GCG GTC Ala Val	3186 GCT CCT Ala Pro	
G. FII		TTG Leu	AAT Asn	$\frac{GGG}{G1}$	GCC Ala	
APPROVED O.G. FIG. BY CLASS SUBC	•	GAT Asp	TAC Tyr	GAA Glu	\mathtt{TAT}	
AFFR ORAFI		CTT Leu	GTG Val	GCA Ala	CGC Arg	
		ACA Thr	GGC Gly	ACA Thr	$_{\rm GGT}$	TAA
<u> </u>		CAA Gln	GCT Ala	CAA Gln	\mathtt{TAT}	TTT Phe
		TGG Trp	CGT Arg	CGC Arg	CAT His	AAG Lys
		CCG	TTG Leu	TTA Leu	AAG Lys	ATG MET
- CE-1-19-0-		2997 ACG Thr	3051 TTT ACC Phe Thr	3105 GCT Ala	3159 CAA GAT Gln Asp	3213 CTT GAA Leu Glu
		TCC	3 TTT Phe	GAG Glu	CAA Gln	CTT Leu
		AAA Lys	AAT Asn	TGG Trp	AGC Ser	GCA Ala
		GCA Ala	GAT Asp	ACT Thr	CTG Leu	TTG
		AAA Lys	ATA AAA Ile Lys	ACC Thr	$\tt GGA \\ \tt G1Y$	CAA Gln
-		ACC	ATA Ile	\mathtt{TAC}	ACA Thr	TAC Tyr
•		GCC Ala	AAC Asn	TAT Tyr	CAT His	AAT Asn
	FIG.5J	CAA Gln	GTA AAC Val Asn	ACC	CAG CAT Gln His	CGC AAT Arg Asn
	FIG	AAA Lys	TAT Tyr	AAT Asn	AAT Asn	GGA G1y

vғо О. G.	CLAS	HAIN
APPROVE	≥	DRAFTSH

DRAFTSHA

FIG.6A

tbpB gene catarrhalis 4223 MοĘ Sequence

ACAT	PTTT	54 TTA Leu	108 CCA Pro	162 GAT Asp	216 GCC Ala	270' GAT Asp
ATGC?	TTAI	TTA	ATT Ile	ACT Thr	AGT Ser	AAA Lys
CCAAA	BAGG/	GTC Val	CCC ATT Pro Ile	GGC GGT ACT Gly Gly Thr	GGC Gly	GAA Glu
racgo	ATCAC	GCC	ACG Thr	GGC Gly	ACA Thr	AAT Asn
raaa:	ACCC?	TCT	CCT	GCT Ala	GGT Gly	GAG AAA AAT GAA AAA Glu Lys Asn Glu Lys
GTAAATT¦GCCGTATTTTGTCTATCATAAATGCATTTATCAAATGCTCAAATAAAT	TGTCAGCATGCCAAAATAGGCATCAACAGACTTTTTAGATAATACCATCAACCCATCAGAGGATTATTTT	ATG <u>AAA CAC ATT CCT TTA ACC ACA CTG TGT GTG GCA ATC TCT GCC GTC TTA TTA</u> MET Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val Leu Leu	CCA CCT GCT CCT Pro Pro Ala Pro	ACT GGT AAT GCT Thr Gly Asn Ala	ACA AAC TCT GGT ACA GGC AGT Thr Asn Ser Gly Thr Gly Ser	GAG Glu
rgc'T(racc <i>i</i>	GCA Ala	CCT	GGT Gly	AAC Asn	GTA CCA ACT Val Pro Thr
CAAAT	ATAAT	GTG Val	CCA	ACT Thr	ACA Thr	CCA Pro
rtat(rTAG?	TGT	AAT Asn	AAC Asn	$_{\rm GGT}$	GTA Val
3CAT	rtrtr	27 CTG Leu	81 TCA Ser	135 GGC GlY	189 GGC G1y	243 GAT Asp
4AAT(AGAC	ACA Thr	$_{\rm GGT}$	ACT Thr	ACA Thr	CAA Gln
rcat?	ZAACZ	ACC	$_{\rm GGT}$	AAT Asn	AAT Asn	$\mathtt{TAT}\\\mathtt{TY} r$
rcta1	SCATO	TTA	AGT Ser	GGT G	$_{\rm GGT}$	AAA Lys
rttg	ATAG(CCT	GGT GGC Gly Gly	TCA Ser	GCA Ala	CCA
3TAT:	CAAAZ	ATT Ile	$\texttt{GGT}\\ \texttt{G1}_{Y}$	$_{\rm G1Y}$	AAT Asn	GAG Glu
יסטפי	TGCC	CAC	TGT Cys	AGC Ser	GCC Ala	CCA Pro
ATT	AGC?	AAA Lys	ACC GCT TGT GGT GGC AGT Thr Ala Cys Gly Gly Ser	AAT GCT AGC GGT TCA GGT Asn Ala Ser Gly Ser Gly	AAT ACA GCC AAT GCA GGT Asn Thr Ala Asn Ala Gly	AAC ACA CCA GAG CCA AAA Asn Thr Pro Glu Pro Lys
GTA?	TGT(ATG MET	ACC Thr	AAT Asn	AAT Asn	AAC Asn

		324 AAA Lys	378 ACC Thr	432 TCG Ser	486 GCG Ala	540 GAT Asp	594 CAG Gln
		AGT Ser	ATT Ile	TTT Phe	GTA Val	TCC Ser	TTT Phe
IG. SUBCLASS		TTG	ATC Ile	CCA Pro	AAT Asn	ATC Ile	GAG Glu
O.G. F		GCT Ala	AAT Asn	TTG Leu	ATG	GAA Glu	CAT His
APPROVED O.G. FIG. BY CLASS SUBCI		ATG	AAA Lys	CCA Pro	AAA Lys	AAA Lys	AGC Ser
		GGC Gly	GAA G1u	TCG	GCA Ala	AAT Asn	AAA Lys
		$\mathtt{TAT}\\\mathtt{TY}r$	GAT Asp.	AAA Lys	ATA Ile	GGT Gly	CGT Arg
		$_{\rm GGT}$	TTA	AAA Lys	\mathtt{TAT}	AAA Lvs	GTG Val
		ATG MET	CCA Pro	GGT Gly	${\tt GGC}$	AAG Lys	GCT Ala
		297 GCC Ala	351 ACG Thr	405 GAA Glu	459 GAT Asp	513 ATT Ile	567 GAA Glu
.D		CCT	GAC Asp	GCA Ala	CTT Leu	AGA Arq	AAA Lys
		GAA Glu	CAA Gln	GTT Val	TTG	GAC Asp	ATC Ile
		CAA Gln	CGA Arq	CAA Gln	AAA Lys	GGT G1y	CAA Gln
		ATT Ile	AAC Asn	AAA Lys	AAT Asn	ATT Ile	AAA Lys
-		TCC	CAC His	GGT AAA AAA CAA Gly Lys Lys Gln	GAA Glu	GCC Ala	GCC Ala
		TCA Ser	CTA Leu		GTA Val	AAT	CTT
•	FIG.6B	AAA GTT Lys Val	ATT AAT CTA CAC AAC CGA Ile Asn Leu His Asn Arg	TTA GAC Leu Asp	TTA GAT GTA GAA AAT Leu Asp Val Glu Asn	GAT AAA AAT GCC ATT GGT Asp Lys Asn Ala Ile Gly	GAA GAA CTT GCC AAA CAA Glu Glu Leu Ala Lys Gln
	FIG	AAA Lys	ATT	TTA	TTA Leu	GAT	GAA Glu

	WO 97/	/32980		17/90			PCT/CA97/0016
LASS		648 ACC Thr	702 AAT Asn	756 GTG Val	810 GAT ASP	864 AGA Arq	918 GCA Ala
O.G. FIG.		ACA Thr	GCG Ala	CCT Pro	CAA Gln	AGA Arq	$_{\rm GGA}$
,		GGA Gly	TTG Leu	GGC Gly	ACA Thr	AAC Asn	\mathtt{TAT}
APPROVED. 8 Y BRAFTSMAN		GAC Asp	TAC Tyr	TTA Leu	CCC Pro	GCC Ala	\mathtt{TAT}
		AAT Asn	TAC Tyr	AAT Asn	TTG Leu	GTT Val	TGG Trp
		TCA Ser	$_{\rm GGT}^{\rm GGT}$	TGG Trp	GAG Glu	ACC GAT Thr Asp	GGC Gly
1		CAT His	\mathtt{TAT}	CTT Leu	AAA Lys	ACC	GCA Ala
		TTT Phe	GAT Asp	AAA Lys	GCC Ala	ATG	CAA G1n
		ATT Ile	GTT Val	GAC Asp	ACC Thr	TTT Phe	TCT Ser
		621 AAA Lys	675 TAT TYr	729 ACA Thr	783 ACG Thr	837 GAC Asp	891 AAC Asn
		AAC Asn	AAA Lys	AAA Lys	ACA Thr	TGG Trp	GAA Glu
		GAA Glu	TTA Leu	GTC Val	GGC Gly	CAT His	AAA Lys
		CTG	GAT Asp	ACC Thr	AAT Asn	GGA Gly	GTG Val
		TCA Ser	CGA Arg	CTA Leu	TAT Tyr	AAA GGA CAT Lys Gly His	GAA Glu
		TCA Ser	ACA Thr	\mathtt{TAT}	TTT Phe	\mathtt{TAT}	AGC
		TTA Leu	ACC Thr	AAT Asn	GTG Val	AAA TAT Lys Tyr	CGA TTT AGC GAA GTG AAA Arg Phe Ser Glu Val Lys
•	.ec	GTA Val	GCA. Ala	GGC G1y	GGT Gly	GTC Val	CGA
•	FIG.6C	CAA Gln	AAA Lys	GAT Asp	$_{\rm G1Y}$	GCG Ala	AAC Asn

GGC AAT Gly Asn

AAG Lys

CAT His

CGC Arg

GAC Asp

CAA Gln

CTA Leu

Asn

AAC

TTT AGT Phe Ser

CTG

AAG Lys

 $\texttt{GGT}\\\texttt{G1}\underline{\texttt{y}}$

ACA Thr

TTA Leu

AAA Lys

AAA Lys

GTT Val

1080

•		972 GAT Asp	1026 GAA Glu	
.Ass		AAA GAA GAC TCT GCC CCT Lys Glu Asp Ser Ala Pro	1026 AAG GAA Lys Glu	
аргиолер O.G. F.I.G. ву CLASS SUBCLASS	с	GCC Ala	TTT Phe	
		TCT Ser	AAT Asn	
APPROVED BY DRAFTSHAH		GAC Asp	GTT Val	
		GAA Glu	ACT Thr	
<u> </u>			TTT Phe	
		ACT Thr	GAG Glu	
		TTA Leu	AGT Ser	
		945 TTA Leu	999 AGC Ser	1053
.0 .0		CGC Arg	CAT His	
		TAC AAC CGC Tyr Asn Arg	GGC Gly	
		$\mathtt{TAC}\\ \mathtt{TY} r$	TAT Tyr	
		GAA Glu	GGT GAA Gly Glu	
		GAT Asp	$_{\rm GGT}$	
		AAA Lys	AGC Ser	
	3.6D	TCA	CAT	
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TCT

GGT Gly

1134 CGC TTC Arg Phe 1188 TTT ACC Phe Thr GAG Glu Asn CCC Pro GGC Gly GGC Gly CAC His AAA Lys CCA Pro AAA Lys CAC His AGC Ser ATC Ile GGGGAAT Asn ACA Thr TAT Tyr GCC Ala GAC Asp TTT Phe GAT Asp AAT Asn GGT Gly 1161 AAT AAA . Asn Lys . 1107 GAC ATC Asp Ile GGT Gly 1215 GAA Glu AGC Ser TAT TYTCTA Leu GCA Ala CGC Arg AGG Arg ACC Thr GAA Glu AAT Asn AAC Asn GCC ACC Thr AAA Lys GCC Ala AGT Ser GAT Asp ACA GGC Gly

> CGT Arg

APPROVED O.C. FIG. BY CLASS SUBCLASS DRAFTSMAN		1296 GGC GTC TTT GGT GCT Gly Val Phe Gly Ala	TTA GAT GCC TAT GCA Leu Asp Ala Tyr Ala	1404 CCA TTT ACC GAA AAA Pro Phe Thr Glu Lys	1458 GGT TCT ACC GTC ATT Gly Ser Thr Val Ile	AAA GAC AAG CCA GAG Lys Asp Lys Pro Glu	1566 ATG GTG AAT GAT GAA GTT AGC GTC MET Val Asn Asp Glu Val Ser Val
		TTT (Phe (ATC I	ACC (Thr 1	TTA (Leu (ACC Thr 1	AAT (
		CTC Leu	GCC Ala	TTC Phe	GTC Val	TTC Phe	ATG GTG MET Val
		AAA Lys	GAA Glu	ACA Thr	TTG	GAA Glu	
The state of the s		AAC Asn	ACC Thr	ACC Thr	AAA Lys	AAT Asn	TTG
		1269 GAC	1323 AAA Lys	1377 GCA Ala	1431 GCC AAA Ala Lys	1485 AAA Lys	1539 ACT Thr
		1 AAT Asn	1 GAA Glu	1 AAC Asn	GCC Ala	ACC Thr	GAG Glu
'ile'		ACC Thr	GAG Glu	AGT Ser	AAT Asn	GCC Ala	GGC Gly
		TTA Leu	GCT Ala	ACA Thr	GGC G1y	GAT Asp	GCG Ala
		TTC	AAA Lys	AAT Asn	TTT Phe	ACT Thr	GAA GCG
-		AAA Lys	AGT Ser	TTT Phe	AAC Asn	CCT	AAC Asn
		$_{\rm GGT}$	GAG Glu	ACA Thr	GAT Asp	GTG Val	ACA AAC Thr Asn
	FIG.6E	GCA Ala	CGA Arg	GGG G1y	CTG	TTG	GCC Ala
•	FIG	CTG	AAA Lys	CTT Leu	CAA Gln	GAT	TCT Ser

1890 GGC AAT Gly Asn

GCA Ala

CAA Gln

 ${\tt GGT} \\ {\tt G1y}$

ACA Thr

ATC Ile

AGC Ser

1863 TTT Phe

> GAC Asp

CAA Gln

CGC Arg

66C

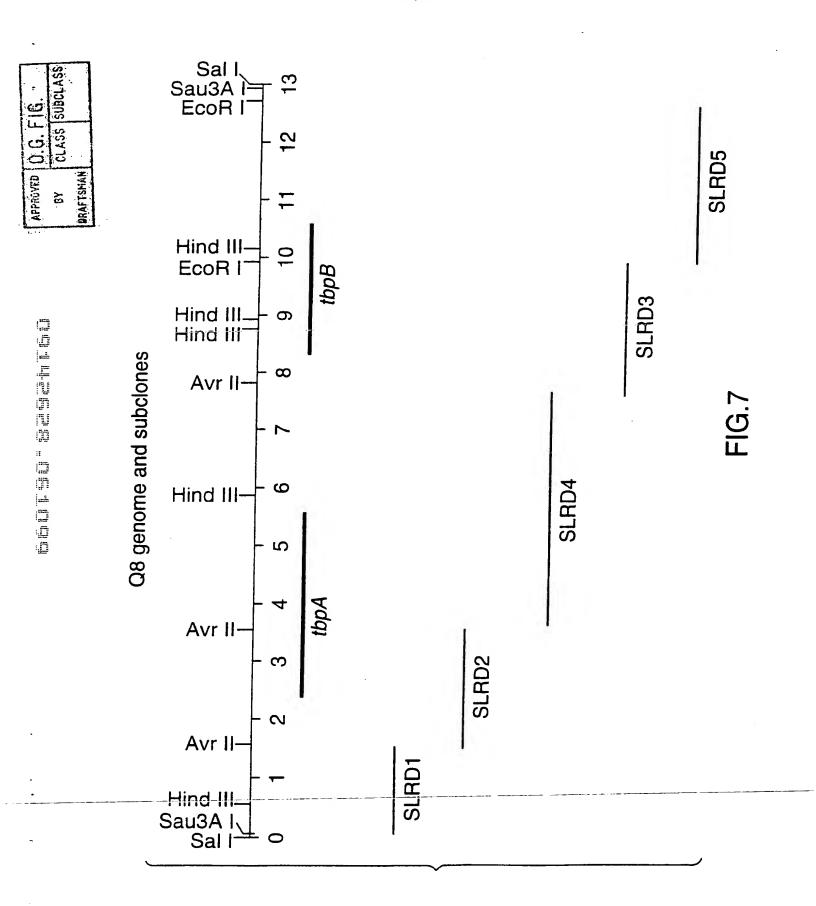
AAA Lys

ACC Thr

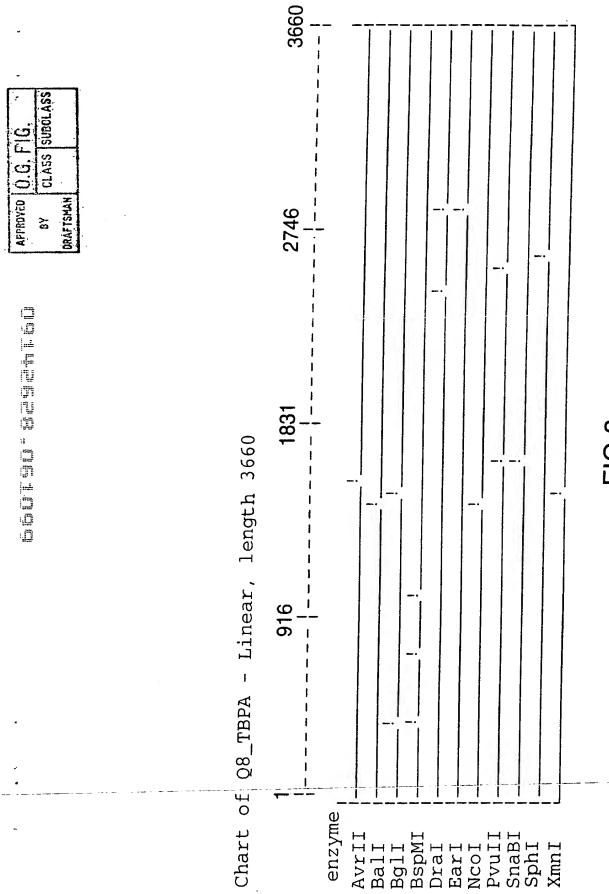
				20,3		
O.G. FIG.	• -	1620 AGT ATC GGT Ser Ile Gly	1674 GGC GAG AAA Gly Glu Lys	1728 GGA TAC ATC Gly Tyr Ile	1782 GCC CAA GAT Ala Gln Asp	1836 AAA CTT ATC Lys Leu Ile
APPROVED O.G. FIG. BY CLASS SUBC		CTT Leu	ACA Thr	GTA Val	GAT Asp	GGT Gly
		GAG Glu	ACC Thr	TGG Trp	ACC Thr	AGC Ser
: true		$_{\rm GGT}$	GCT Ala	AAC Asn	TTT Phe	GTC Val
		TTT	ACC Thr	GGG	AGC Ser	TCA Ser
		CTA AAA Leu Lys	CGC Arg	TTG	AAA Lys	AAA Lys
		CTA <u>Leu</u>	GAA Glu	\mathtt{TAT}	GGA Gly	AAT Asn
		1593 GAA TAC CTA AAA TTT Glu Tyr Leu Lys Phe	1647 GGC G1y	1701 AAA Lys	1755 ACA Thr	1809 GGA G1y
		GAA Glu	CAA Gln	GCC Ala	1 GGC G1Y	1 TTT Phe
		TTT	TTA Leu	ACA Thr	ACG Thr	GAT Asp
		AAC Asn	TTT Phe	$_{\rm GGC}$	$\texttt{GGA}\\ \texttt{G1}\underline{\texttt{y}}$	ATT Ile
		AAA Lys	GTC Val	ACA Thr	ACA Th <i>r</i>	GAC Asp
-		TAT GGC AAA AAC TTT Tyr Gly Lys Asn Phe	AGC Ser	CCA ACC Pro Thr	GAC Asp	TTT Phe
		TAT TVĽ	CAT	CCA Pro	AAG Lys	GAT
	.6F	AAA ACC TAT GGC AAA AAC Lys Thr Tyr Gly Lys Asn	AGC Ser	GTA	GGA Gly	GCT Ala
	FIG.6F	AAA Lys	$_{\rm G1Y}^{\rm GGT}$	GCC Ala	ACA Thr	GTT Val

0.G. FIG.	CLASS SUBCLASS	
APPROVED), (9)	BRAFTSMAH

1944	1998	2052	2106
TAC AAG ATA	ACA GGG	CAC AAC GCC	GTT AAG
Tyr Lys Ile	Thr Gly	His Asn Ala	Val Lys
AA(Ly:		AA(Ası	GT
$\mathtt{TAC} \\ \mathtt{TYr}$	GTT	CAC	CAA GAA (
	Val	His	Gln Glu
GCG GAC GCA GGA GGC	AAT	ACA	CAA
Ala Asp Ala Gly Gly	Asn	Thr	Gln
GGA	GCC	TTT	CAA
Gly	Ala	Phe	G1n
GCA	GAT	TCA TTT Z	ACA AAA AGA CAA
Ala	Asp		Thr Lys Arg Gln
GAC	AAA	GGG	AAA.
Asp	Lys		Lys
GCG	ATC	GGC	
Ala	Ile	Gly	
AAA	GCC	ATG	GGC
Lys	Ala	MET	Gly
1917	1971	2025	2079
ACC ACC	TCC ATC GCC ATC AAA GAT GCC AAT	GAG	GTC TTT
Thr Thr	Ser Ile Ala Ile Lys Asp Ala Asn	Glu	Val Phe
ACC Thr	TCC Ser	2025 GCA AAC GAG Ala Asn Glu	GTC Val
AGC	AAA		GTG
Ser	Lys		Val
GCC	$_{\rm GGC}$	CCA AAT	GCC TCT
Ala		Pro Asn	Ala Ser
ACA GCC	ACA (Thr	CCA	GCC
Thr Ala		Pro	Ala
GGG	AGT	$_{\rm GGT}$	AAA (
Gly	Ser		Lys
ACA Thr	AGC Ser	$\mathtt{TAT}\\\mathtt{T}Yx$	AGC Ser
TGG	GAT TCT AGC Asp Ser Ser	TTT Phe	GAC AGC ASP Ser
GGC	GAT	GGC	GAT
Gly		Gly	Asp



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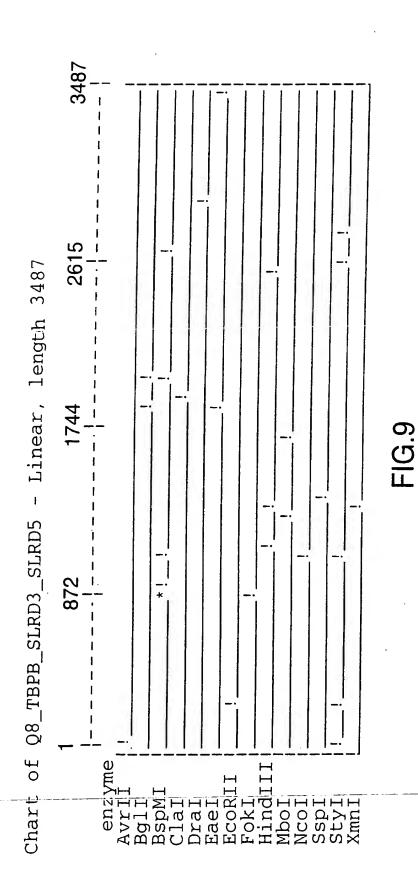
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APPROVED O.G. FIG.



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-		APPROVED O.G. FIG: BY CLASS SUBCLASS BRAFTSMAH
FIG.10A		
08 tbpA ger	08 tbpA gene sequence	
AATTG	AATTGATACAAAATGGTTTGTATTATCACT 20 30 TGTATTGTATTAAAT	ТТТАСТТАТТТТТ 50 60
ACAAAQ	CTATACACTAAATCAAAATTAAT 90 70 CACTTGGTTGGTG	T T T A G C A A G C A A A 110
TGGTTA	TTTTGGTAACAATTAAGTTCTTA 130 140 AAACGATACAGCTCA AAAACGATACAG	TAAACAGATGGTT 170
TTTGGC	ATCTTCAATTGATGCCTGCCTTG 210 190 TGATTGGTTGGTGT 220	АТТGАТGТАТССА 230
AGTACA	MET A A A G C C A A C A G G T G G T C A T T G A T G 250 250 260 270	

APPROVED O.G. FIG. .
BY CLASS SUBCLASS

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ASN GIN SER LYS SER LYS LYS SER LYS AATCAATCCAAAAATCCAAAA 280 290 300	LEU TTG 330 LEU ASN ILE THR GIN VAL ALA LEU CTTAACATCACGCAGGTGGCACTG 340	ALA GLU ALA G C G A G G C A 390 THR ASP LYS THR ASN LEU VAL VAL LEU A C A G A T A A G A C C T T G T T G T C T T G 400	LYS LYS ASN A A G A A A A A C 450 ALA ARG LYS ALA ASN GLU VAL THR GLY LEU G C C G T A A A G C C A A C G A A G T T A C A G G G C T T 460
LYS LYS AAAAAT)	ASN ILE THR PACATCACG	ASN A A A C C	ASN GLU
ASN GIN SER LYS AATCAATCCAA 280	TGCCTTGTCT 320 GLY LEU GGTCTG	LYS L A A G (380	A ALA A G C G 440
	GIN VAL LEU LYS LEU SER	ALA ASIN THR THR ALA ASPGCAACGACGAT	ASP GLU THR VAL VAL THR GATGAA CTGTTGTAACA 430
	GLN VAL CAAGTA	ALA ASN GCAAAC	ASP GLU GATGAA

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APPROVED O. G. FIG. BY CLASS SUBCLASS DRAFTSMAN		LEU ASN ILE ARG ASP STAAACATTCGAGAC 530 540	GLY ALA SER SER GLY 3 G G C A A G C T C A G G C 590 600	ASP GLY ILE ASN GLN 3 A T G G C A T C A A T C A A 650	
		GLY LYS VAL VAL LYS THR ALA GLU THR ILE GGTAAGGTCAAAACTGCCGAGACCATC 510 490 ASN LYS GLU GLN VAL LEU ASN ILE ARG ASP AATAAGAACAAGTGCTAAACATTCGAGAC 520 530	LEU THR ARG TYR ASP PRO GLY ILE ALA VAL TTAACA CGCTATGACCCTGGCATTGCTGTG 570 550 VAL GLU GLN GLY ARG GLY ALA SER SER GLY GTTGAGCAAGGTCGTGGGCAAGCTCAGGC 580 580 580	TYR SER ILE ARG GLY MET ASP LYS ASN ARG TATTCT ATTCGTGGTATGGATAAAATCGT 630 VAL ALA VAL LEU VAL ASP GLY ILE ASN GLN GTGGCGTTGGTTCAATCAA 640 650	ALA GIN HIS TYR ALA LEU GIN GLY PRO VAL GCCCAGCACTATGCCCTACAAGGCCCTGTG 670 680 690
-	FIG.10C	GGTAAG	LEU THR TTAACA	TYR SER	ALA GIN GCCCAG

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C G CGEU ASN

AAT GAA TAC Ø G A Ø A T K Ø G A C

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CCAAA GCATTT GTG TCT

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ATA CAGGGT TTTTTA EEG TAT AGC SER 出 TCTTTTP 950 'GATGCC1 1010 CCAAAA 盟 SER 88 TACAAGGCACATGAT GACCCAAATAAC AAGGCAGGT ASP GLYALA HIS ASN GAA GTGCAACC GTGCAGCA LYS ALA OLD OLD GCAGGC CAA ALA GLY GIN LYS ACT GGT AAT VAL AATTCT AGAGCG CGCCGT T G G TALA ARG ARG ASIN AA AATGTGCCA 1090 G T T TACACCGAC GAT ASP WAL ATGG E 讯 出 AGTT GAA Z ASN ASIN A A ΑT Ø ں AGC AAT

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ALA CYS ALA ALA GLY GLY GIN THR LYS LEU G C G T G T G C T G C C G G T C A A A C T C 1120 1130 1140	ALA LYS PRO THR ASN VAL ARG ASP LYS G C T A A G C C A A T G T G C G T G A T A A G 1150 VAL ASN VAL LYS ASP TYR THR GLY PRO ASN G T C A A T G T C A A A G A T T A T A C A G G T C C T A A C 1180	EU LEU LEU ARG PRO GLY TACTGCTTCGCCCAGGTT 1250	LEU ASN ASP LYS HIS TYR VAL GLY GLY CTAAACGATAAGCACTATGTCGGTGGT 1290 VAL TYR GLU ILE THR LYS GIN ASN TYR ALA GTGTATGAAATCACCAAACAAACTACGCC
	ALA LYS PI S C T A A G C (LEU ILE PE TTATCC 1210	LEU ASN AS TAAACG1

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.G. F1G.	CLASS SUBCLASS	
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TRP PHE ASP ASP VAL ARG VAL SER TYR A T G G T T T G A T G T G C G T G T C T T A T 1570 ASP ISSO ASP ISS GIN THR ASN THR HIS CYS SER THR TYR PRO 3 A C C A A C A C G C A C T G T T C A A C C G 1650 HIS IIE ASP C A C A T G A G A A C A T G T G T C A A C A T G A C 1640 HIS IIE ASP I A A A C C T T T T C G T A A A G A G G T G A T 1710 1710	GLU TYR VAL TYR ASP SER LYS GLY GLU ASN	TYR	ASP LYS GIN ASP ILE THR LEU ARG SER GIN	PRO	HIS ILE ASP LYS ASN CYS THR PRO ASP VAL	ASP
	GAATATGTTTATGACAGCAAAGGTGAAAAT	P.A.T	GACAAGACATTACGCTACGTAGCCAG	2 C G	CACATTGACAAAATTGTACGCCTGATGTC	3 A T
	1540 1550	1590	1600 1620	1650	1660 1680	1710
		ASP ASP VAL ARG VAL SEGATGATGTCTC70	ASP LY G A C A A	THR HIS CYS SER THR TY ACGCACTGTTCAACCTA 30	HIS I CACAT	PHE SER VAL LYS GLU VA TTTCGGTAAAAGAGGT 1700

AAA

			33/90		
,		LYS MET ALA A A A G G C A 1770 LEU GLY ASN THR HIS HIS ILE ASN LEU T G G C A A T A C G C A T C A C A T C T G T 1780 1780 1800	ASN SER SER A A T T C A A G C 1830 LEU SER ARG GLU ASP TYR ARG LEU ALA THR C T T A G C C G T G A A G A T T A T C G T T T G G C A A C C 1840 1850	ASP TYR THR GATTACACC 1890 PRO PRO SER ASN PRO LEU PRO ASP LYS PHE CCACCAAGTAAGTTT 1900 1900	
SCLASS		ASN A A T	ALA 3 C A	LYS A A G	
APPROVED 0.G. FIG. BY CLASS SUBCLASS ORAFISMAN		ILE \ T C F	LEU	ASP 3 A T A	
PH CL A		S C A	. E	A G	
APPROVED BY DRAFTSMAH		HIS C A C 1790	ARG C G T 1850	PRO 3 C C A C 1910	
		HIS CAT	TYR T A T	LEU TTG	
		HIS CAT	ASP TYR 3 A T T A T	PRO	
		THR A C G C	GLU SAAG	ASN	
		A 0 0 1 TH 1 A (E C C C C C C C C C C C C C C C C C C C	IR 2 C 390 3 T A A 1900	. V O
		ALA G C A 1770 ASN 178	SER AGC 1830 ARG CGT	THR A C C 1890 SER A G T 190	PRO C C C 1950
		LYS LYS MET ALA A A A A A A T G G C A 1760 LEU GLY ASN T G G G C A A T	PHE ASN SER SER TTCAAGC 1820 LEU SER ARG CTTAGCCGT	LEU ASP TYR THR CTTGATTACACC 1880 PRO PRO SER CCACCAAGT	ASN ASN ARG PRO AACAACAGACCC 1940 1950
		LYS AAAA LEU TTG	ASN A A T T LEU C T T	ASP G A T 7 PRO C C A 0	ASN ARG AACAGA
12 12 12		LYS I I A A A I 60	5. U	<u>.</u> H	N A C A
		LY 2 A A 1760	PHE A T T C 1820	LEU A C T T 1880	
		ASN A A (LYS A A A	LYS A A <i>P</i>	SER T C 7
		PHE T T	ASP A T	A A A	GLY 3 G T
		P. C. T	R T G	R (JU (
•		LA VI C C G 7 1750	C T 78	TTT 78870	.Е. LE ГТТ 1 1930
		ALA G C 1	GLY G G G	SER T C 1	ILE A T
<u> </u>	10.	ILE LYS ALA VAL PHE ASN A T C A A G C C G T C T T T A A C 1750	GIN VAL GLY TYR ASP LYS CAAGTTGGCTATGATAAA 1810	HIS GIN SER TYR GIN LYS CATCAAAAA 1870	LYS PRO ILLE LLEU GLY SER A A G C C C A T T T T A G G T T C A 1930
~	FIG. 10.	T C ;	JIN A A (IIS A T (YS A G (
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0,G. FIG.	CLASS SUBCLASS	
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CAT**9** TAT TATGGT GLY CTTGATGCT B Jec ATT

ALA GIN PRO PRO

AAA ີ ປ ບ AAC G T CCACAG GAC ASP

ATC AACTTTGCC TATCAA TYR AGC

AAT ACC AACCAA TAC GAGCAA 0 6 6 7

AAGATTGATTATCAAGCC GAT ASP

GAC

MAL

ALA

GIN

ASIN ASIN GIN CAA

AACAGCACC AACCCC CAA GATAAA

AGT CAA AAA AAAATC CCCTTTGAG PRO AAA CTA B

TATAGC 2340

AAA

AAATGT*P* 2330

AAAGAT

TGAT 7 2360

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TAT

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A C A G C 1 2350

APPROVED O.G. FIG.

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	.#.	Marie Marie	
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 	T T A 2220		THR A C G 2280		SER
d d d	ASF G A T		G G C		TYR
DA.I	A A A		LYS A A A		LYS
ፈ ሊ	r T A T 7 2210		ASN A A T 2270		CYS
A.1.A	CT C		ALA 3 C C 7		LYS
NS S	ATC		ASIN A A C (ASP
H.	TT		GLN : A A A		ASP
GLU ILE ASP AGATAGAC 2190 ARG LEU GLY PHE ASN ALA TWR IVS ASD ITHI	AGACTGGGCTTTAATAAAGATTA 2200 2210 2220	ASP 3 A C 2250	ASN SER GIN GIN ASN ALA ASN LYS GLY THR A A C A G C C A A C A C G C C A A T A A G G C A C G 2280	THR A C T 2310	
TYR ASP GLU ILE ASP TACGACGAGATAGAC 2180 ARG LEU GLY	0 L C	GLY TRP THR ASN ASP GGTTGGACTAATGAC 2240	SER AGC(PRO ASN GIN ALA THR CCAAATCAAGCAACT 2300 2310	VAL
GLU 3 A G A ARG	4 G A (THR	ASN A A C A	GIN CAAC	VAL
ASP C G A C C 2180	7	TRP T G G A 2240	į	ASN 1 A A T C 2300	
TYR ACG 21		GLY G T T 22		PRO CAA 23	
LYS A A T		ALA C G G		SIN A G C	
ELU] A A A		TRP 7		TYR (A T C	
LEU GLY GIN GLU LYS TTGGGCAAGAAAA 2170		ARG ASIN GLU TRP ALA CGCAACGAATGGGCG 2230		ASP ASN ILE TYR GIN GATAATATCTATCAG 2290	
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G C G		ASN A A C		ASN A A T	
LEU PTG		ARG 2 G C.		ASP 3 A T	
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COLTAGE RESERVED

	36	/90	101/010/1/00105
THR ARG HIS ILE SER GLY ASP ASN TYR PHE ACTCGCCACATCAGCGGTGATAATTTC 2380 2390 2400	ILE ALA LEU LYS ASP ASN MET THR ILE ASN A T C G C T T T A A A G A C A T G A C C A T C A A T 2420 LYS TYR VAL ASP LEU GLY LEU GLY ALA ARG A A A T A T G T T G G G C T G G T G C T C G C 2460	TYR ASP ARG ILE LYS HIS LYS SER ASP VAL TATGACAGAATCACAAATCTGATGTG 2490 2470 PRO LEU VAL ASP ASN SER ALA SER ASN GIN CCTTTGGTAGACAACAGCAACAG	LEU SER TRP ASN PHE GLY VAL VAL VAL LYS CTGTCTTTGGATTTTTGGCGTGGTCAAG 2550 2530 PRO THR ASN TRP LEU ASP ILE ALA TYR ARG CCCACCAATTGGCTGGACATCGCTTATAGA 2580

2760

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WO	97/	270	RC

	WO 97/32980		37/90		
	VAL	2640	THR A C T 2700		LEU
ASS	GLY)))	GIN C A G		THR
ss subclass	ARG PHE GLY VAL	.	GLN C A G		ALA
APPROVED O.G. FIG. BY CLASS SUBCL	ARG	2630	TYR ILE CYS GLN GLN ACATTTGTCAGCAG 2690		GLY
APPROVEO BY DRAFISHAN	GLU GLU		ILE ATT 2		ILE
أسيدا	GLY GLU))	TYR T A C		GEN
	TYR	0	TYR T A T 30		GIN
	PRO SER PHE CCAAGTTTT 2610 SER GLU MET TYR GLY GLU ARG PHE GLY VAL TCTGAAATGTATGGCGAACGCTTTGGCGTA	2620 CYS T G T 2670	LYS GLY LEU TYR TYR ILE CYS GLN GLN THR AAGGGTCTTTATACATTTGTCAGCAGACT 2680 2700	LYS A A A 2730	SER PHE ASN
	PRO SER CAAGT SER GLU	C C C	LYS GLY A G G G T	GLU GAA	田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田田
	PRO SER PHE CCAAGTTTT 2610 SER GLU MET TCTGAAATG	26 HIS GLY CYS CATGGCTGT 2670	LYS A A G		SE C

AGCTC GCAAGGCTTTCGCATGCCAAGTTTT 2610 2610

MET

ARG

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GLY

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SER

TCCTTTAACCAAGAAATCGGAGCGACTTTA GLN ASIN 2730 GTCCAT CAAACCAAGCTAAAACCTGAAAAA 2730 出出 SER

2750 CATAACCACTTAGGCAGTCTTGAGGTTAGT 2790 OE CE SE GLY IEI ASIN

FIG. 10M

DOTLESS WEST TOOL

SUBSTITUTE SHEET (RULE 26)

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PROVED 0.G. FIG.	CLASS SUBCLASS	
APPROVED	} 8	DRAFTSMAN

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TYR PHE LYS ASN ARG TYR THR ASP LEU ILE	VAL GLY LYS SER GLU GLU ILE ARG THR LEU	THR GIN GLY ASP ASN ALA GLY LYS GLN ARG	GLY LYS GLY ASP LEU GLY PHE HIS ASN GLY	GIN ASP AIA ASP LEU THR GLY ILE ASN ILE	LEU GLY ARG LEU ASP LEU ASN ALA VAL ASN	SER ARG LEU PRO TYR GLY LEU TYR SER THR
TATTTAAAATCGCTATACCGATTTGATT	GTTGGTAAAAGAGATTAGAACCCTA	A C C C A A G G T G A T A T G C A G G C A A A C A G G T	GGTAAAGGTGATTTGGGCTTTCATAATGGG	CAAGATGCTGATTTGACAGGCATTAACATT	CTTGGCAGACTTGACCTAAACGCTGTCAAT	AGTCGCCTTCCCTATGGATTACTCAACA
2800 2810 2820	2830 2840 2850	2860 2870 2880	2890 2900 2900	2920 2930 2940	2950 2950	2980 2990 3000
-	VAL GLY GTTGGT?		GLY LYS GGTAAAC	, <u>-</u>	LEU GLY CTTGGG2	

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APPROVED O.G. FIG. BY CLASS SUBCLASS DRAFTSMAN			LYS THR LEU ASN PRO THR LEU ALA GLY THR A A A C C T T A A A C C C A A C T T T G G C A G G A A C A 3040		ARG TYR VAL VAL GLY LEU GLY TYR ASP ALA CGTTATGTGGTGGGCTTGGCTATGATGCC 3100 3120		PHE THR HIS SER ASP ALA LYS ASN PRO SER TTTACCCATTCTGATGCCAAAAATCCAAGC 3160 3170 3180	
	2	LEU ALA TYR ASN LYS VAL ASP VAL LYS GLY CTGGCTTATAACAAGTTGATGTTAAAGGA 3020 3030	LYS THR LEU ASN PR AAAACCTTAAACCC 3040	ASN ILE LEU PHE ASP ALA ILE GIN PRO SER A A C A T A C T G T T T G A T G C C A T C T 3070 3090	ARG TYR VAL VAL GLY CGTTATGTGGGG	PRO SER GIN LYS TRP GLY ALA ASN ALA ILE CCAAGCCAAAATGGGGAGCAAACGCCATA 3130	PHE THR HIS SER ASP TTTACCCATTCTGAT 3160	GLU LEU LEU ALA ASP LYS ASN LEU GLY ASN GAGCTTTTGGCAGATAAGAACTTAGGTAAT 3190 3200 3210
. (FIG.100	LEU AL CTGGC		ASN ILL AACAT		PRO SER CCAAG		GLU LEU GAGCT

	***************************************		40/90	PC1/CA9//00103
TO THE	GLY ASN ILE GLN THR LYS GIN ALA THR LYS GGCAACATTCAAACAAAAAAAAAAAAAA	IYR VAL ASN ATGTAAA	TYR THR THR TRP GLU ATTACACCACTTGGGAGG	ARG GIN THR ALA GLU GLY ALA VAL ASN C A A A C A G C A A G G G C G G T C A A T 3370 3370 GIN HIS THR GLY LEU SER GLN ASP LYS HIS C A G C A T A C A G A C A G A T A A G C A T A A G A T A C A G A C A G A T A A G A T A A G A T A A G A T A A G A T A A G A T A A G A T A C A G A T A C A G A T A A G A T A A G A T A C A C A G A T A C A C A C A C A C A C A C A C A C

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	W	O 97/32980		41/90		PCT/CA97/00163
CD TENTUMENT OF THE STATE OF TH	FIG.10Q	TYR GLM ARG TYR ALA ALA PRO GLY ARG ASN TATGGTCGCTCTGGACGCAAT 3430 TYR GLN LEU ALA LEU GLU MET LYS PHE *** TACCAATTGGCACTTGAAATGAAGTTAAA	3470	CCAGTGGCTTTGATGTGATC 3500 3510 3490 3500 CCAATCATCAACCAATGAATAAAGCCCCCATCT 3520 3530 3530	ACCATGAGGGTTTATTTATCATCGCTGA 3570 3550 GTATGCTCTTAGCGGTCATCAGATTA 3500 3600	GTCATTAATTAGCGATTAATTA 3630 GTAATCACGCTGCTTTGATGATTAAG 3640 3650 3660
•	FIG.	TYR T A T	3480	C C A	ACC	G T C

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APPROVED O.G. FIG. BY CLASS SUBCLASS DRAFTSMAH		ATTACCCAAATGCC 50	C A C A A G A C C C A T C T 110	G G C G G C G G T C T T 170	C A A A C C T A A C C A G C 230	TTTGGCACAGAGAC 290
	A Q8 tbpB Sequence.	ACAGTAACACTTTATAC 20 AGCACATTGATTT	CTATTATCTTTGGGGGCAGACTTT 70 80 90 TATGATGAAAGTGC 100	CTATGAGCGTCGTGGCATACGCACA 130 140 GCTTGGGGCAAGAAT	CGTGCCCAAATCAGCATCAACAAA 190 210 CGCCATTACCAAGGAG	CAAATTCGCCAGGATAAACAGATG 250 270 CAAGCGTCTTTATCGC
•	FIG.11A	CCTAGGGCTG	ACACG	GACAG	T C A A G	GGTGGA

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G.11B	CACACGCCTG 330 310 ACCATCAGCACAAAAAAAAA 340 350 350	ATCAAAGGCAAATTATCACAAAATCAA 390 370 ATGTTGTTGAGTTGGAGTTTGAGTGAG	GAȚAAGCATGCCTACTTTGTTTTT 450 450 GTAAAAAAATGTACCATCATAGACAATATC 480	AAAAAAAAAAT 490 510 TTATGATAATTGTTATGTTATT 540 530 540	TATCAATGTAAATTTGCCGTATTTTGT 570 570 CCATCATAAACGCATTTATCAAATGCTCAA 580 590
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FIG.11D SN ALA GLY THR GLY GLY ALA ASN SER ATGCT GGCGGTACTGCAAACTCTG 850 860 870	GLY ALA GLY ASN ALA GLY GLY THR GLY GLY A GTGCAGGTAATGCTGGCGGTG 880 890 900	LA ASN SER GLY ALA GLY SER ALA SER THR CAAACTCTGGTGCAGTGCCAGCACAC 930	PRO GLU PRO LYS TYR LYS ASP VAL PRO THR A CAGAACCAAAATATAAAGATGTGCCAACCG 940 950	SP GLU ASN LYS ALA GLU VAL SER GLY A T G A A A A A A A G C T G A A G T T T C A G G C A 970 980 990	ILE GIN GLU PRO ALA MET GLY TYR GLY VAL G TTCAAGAACCTGCCATGGGTTATGGCGTGG 1000 1010 1020	LU LEU LYS LEU ARG ASN TRP ILE PRO GIN A A T T A A G C T T C G T A A C T G G A T A C C A C A A G 1030 1040 1050
FIG.11D SN ALA C ATGCTG		LA A. CAA.		SP G ATG		LU LI AAT

APPROVED O.G. FIG. . . BY CLASS SUBCLASS

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LU HIS ALA LYS ILE ASN THR A A A C A T G C C A A A T C A A T A C A A 1070	ASP VAL VAL LYS LEU GLU GLY ASP LEU TGATGTTGTAAACTTGAAGGTGACTTGA 1110 LYS HIS ASN PRO PHE ASP ASN SER ILE TRP G AGCATAATCCATTTGACAACTCTATTGGC 1140	ASN ILE LYS ASN SER LYS GLU VAL GIN A A A C A T C A A A G A A G T A C A A A 1170 THR VAL TYR ASN GIN GLU LYS GIN ASN ILE G C T G T T T A C A A G A G A A A A A A C A T T G 1180 1190 1200	ASP GIN ILE LYS ARG GLU ASN LYS GIN AGATCAAAAGAAATAACAAC 1230 ARG PRO ASP LYS LYS LEU ASP ASP VAL ALA L GCCTGACAAAAACTTGATGACGTGCAC 1260 1260
	VAL 3 T T 1	ILE 1 1 C	A A A 1
	ASP TGAT	ASN A A A C P	ASP AGATIO

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LEU L TTGA CTTGCTAAACCCATTT AAAA 园 CLASS SUBCLASS CCAAAG ₽ CGTGA ASP APPROVED O.G. FIG. PRO ARG BRAFISHAN CAGGTTATTCTAATATCATT <u>}-</u> CGC1 ALA ARG GCA GAA ASS ACCGTCTAACA AGCAGAATAAA LYS GTTCTTGATG TCACATGATA TATCGCT GGTGCTTTAT ASIN B TYR 国 ARG GEN ATT ASP N U GAT (GAAAAA A A A A T A T T A A T T A T T A T 1330 1340 TCTGGTTAT 1280 1400 TYR TTT A G GGT TACAAGCTTATATT Z U AAAACT TGCGT ASIN M FIG. 11F GCT GAA AGTAT

APPROVED 10.G. F.IG.

BRAFTSMAH

CAAT TTTATCAAGGTACACAA GLY

TATAAAGGCA LYS AAG TCTCAAGTT 1510 TGGGATTTTATG

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ACCGATGCCAAAAAG

GGTACATCGC 国 回

TCATT1

CAA

GAT CTTGCTGGT AACGT

CGTTATAGTGCAA

园 GAA 3 ACCAT

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AAT CTGATGAGAAAACAAACCAGAT 1660 1670

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ED E	WO	HIS SER SER GLU PHE CATAGCAGTTTA 1700 1710	THR VAL ASP PHE SER LYS LYS SER LEU LYS G CGGTAGATTTTAGTAAAAGAGCCTAAAAG 1720 1730 1740	LY GLU LEU SER SER ASN ILE GIN ASP GLY GTGAGCTGTCTAGTAACATACAAGACGGCC 1750 1750 1760 1760	ER VAL ASN LYS THR LYS ARG T GTGTTAATAAACCAAACGCT 0 1790	TYR GLY ASN CTACGGCAAC 0 183	AKG PHE ARG GLY SER ALA THR ALA SER ASP T GCTTCCGTGGCAGTGCCACCGCAAGCGATA 1840 1850 3	LYS HIS PRO CAAACACCCT 0 1890
		GLU TYR GLY 3 A A T A T G G T C 1690		SER SER T CTAGTA		ASP ALA ASN ILE GATGCCAATAT 1810		LA SER] CAAGCA 0
-	_	GLU T AAT, 169		LEU SI CTGT (175(ILE ASE TCGA 1810		alu ala A A G C 1870
	FIG.11H	SN GLY ACGGTG		LY GLU GTGAGC		YR ASP ILE A T G A C A T C		HR THR GLU ALA SER LYS SER CAACAGAAGCAAAG

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PHE THR SER ASP ALA LYS ASN SER LEU GLU GTU GTU GTU GTU GTU GTU GTU GTU GTU GT	LY GLY PHE TYR GLY PRO ASN ALA GLU GLU G C G G T T T T A T G G A C C C C A G G A G C 1950 1930 LEU ALA GLY LYS PHE LEU THR ASN ASP ASN 1.	TGGCAGGTAAATTCCTAACCAATGACA 1960	YS LEU PHE GLY VAL PHE GLY ALA LYS ARG A A C T C T T T G G T G C T A A A C G A G 1990 2000 2010	GLU SER GLU ALA LYS GLU LYS THR GLU ALA I AGAGTGAAGCTAAGGAAAAACCGAAGCCA 2020 2030 2040	LE LEU ASP ALA TYR ALA LEU GLY THR PHE TCTTAGATGCACTTGGGACATTTA 2050 2060 2060	ASN LYS PRO GLY THR THR ASN PRO ALA PHE TATA A C C T G G T A C G A C C G C C T T T A 2080 2090 2100
	ECGG GCGG		YS LEI AACT		LE LEI TCTT	
	-				. —	

			31,30		
APFROVED O.C. F.IG. BY CLASS SUBCLASS ORAFTSHAH		WAL LEU GLY S GGTCTTGGGTT 0 2160	PHE LYS GLU LATICAAAGAAO	ASP GLU VAL ILE V ATGAAGTTATCG 2270	
		HR ALA ASN SER LYS LYS GLU LEU ASP ASN CCGCT A A C A G C A A A A A A G A A C T G G A T A A C T 2110 2120 2130 PHE GLY ASN ALA LYS LYS LEU VAL LEU GLY ST C T T G G C A T G C C A A A A A A G T T G G G T T 2160	ER THR VAL ILE ASP LEU VAL PRO THR GLY CTACCGTCGTG 2190 2170 ALA THR LYS ASP VAL ASN GLU PHE LYS GLU 1 CCACCAAAGATGTCAATGAATTCAAAGAAA 2220	LYS SER ALA THR ASN LYS ALA GLY A A G T C T G C C A C A A C A A G C G G C G 2230 2230 GLU THR LEU MET VAL ASN A G A C T T T G A T G G T G A A T G 2260	AL LYS THR TYR GLY TYR GLY ARG ASN PHE TCAAAACCTATGGCTATGGCAGAAACTTTG 2290 2300 2310
•	FIG.11J	HR ALA CCGCT	ER THR CTACC	YS PRO AGCCA	AL LYS TCAAA

APPROVED 0:G, FIG.

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GLU TYR LEU LYS PHE GLY GLU LEU SER ILE G AATACCTAAATTTGGTGAGCTTAGTATCG 2320 2330 2340	LY GLY SER HIS SER VAL PHE LEU GIN GLY GTGGTAGCCATAGCGTCTTTTTACAAGGCG 2370 2350 GLU ARG THR ALA GLU LYS ALA VAL PRO THR G AACGCACCGCTGAGAAGCCGTACCAACCG 2380 2390 2400	IU GLY THR ALA LYS TYR LEU GLY ASN TRP A A G G C A A C T G G G A A C T G G G 2430 VAL GLY TYR ILE THR GLY LYS ASP THR GLY T T A G G A T A C A T C A C G G A C A C A G G A A 2460 2460	HR SER THR GLY LYS SER PHE ASN GLU ALA CGAGCACACAGGAAAAAGCTTTAATGAGGCCC 2490 2470 GLN ASP ILE ALA ASP PHE ASP PHE GAACTTTG 2500 2500
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H LYS LYS AAATCA SB、 AGAGA ARG

AAACTGACCA AAAGGC 2540

CCCAAGGCCGCCAAGACCCTGTATTAACA ASP GLY G 呂

GGTCAAATCGCAGGTAATGGCTGGA GLY ASIN 2600 ALA GIN

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ATAGATTCTAGCAGTA 2670 SE THE SER 2660 ASP

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GGCTACAAG 2650

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APPROVED O G, FIG. BY CLASS SUBCLASS BRAFTSMAN	SER PHE THR HIS A TCATTTACACACG 2750 2760	GLU GLU VAL LYS * GAAGAAGTTAAGT 2810	A T C A A A C A T G A A T 2870 2880	G G C A G A T G A T G A G 2930	G T G G T G T T A T C A C 2990
	ALA ASN GLU MET GLY GLY CLY CLY CLY CLY CLY CLY CLY CLY CLY C	SP THR ASP ASP SER LYS ALA SER VAL VAL A T G A C A G T A A A G C C T C T G T G G T C T 2770 2770 PHE GLY THR LYS ARG GIN T T G G C A C A A A A G A C A A 2800	TTAAACACAATGCTTGGTTCGGCT 2830 2840 GATGGGATTGACGCTTA GATGGGATTGACGCTTA	GATTAAGATAAACCCAAGCCATGCCAA 2890 2910 TGATTGATAGCAACGAT	ТСА ТТАТСТ G C C А Т Т А Т Т А Т Т G С Т Т А А 2970 2950 Т Т А Т Т G С С Т Т G G С А Т Т Т G С Т Т G T С А Т Т Т G 2980
•	FIG. 11M	SP THR A TA C C G	** AGTAAT	GATTAA	ТТТГСА

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IIN APTROVED O.G. FIG. Proposed O.G. FIG. PRAFFSMA SOLO 3020 3030 TTAAATGATATTAATGAGGTTA 3040 3050 3060	GGTCATGGTTTTCATGATTATTTAA 3090 CTTATAATGCGTTAGCAAAAG 3110 CTGAAGCTATGGTGAT 3130 3140 TGTGCAAAGATGGTCAAAAAAAATCGGT 3160 3170	ATGGTTCTGTT 3210 AATGATAATAACGGCCAAGCCA 3220	Т G C C A A G T T G T T-G C C G A C C T C T C A G A A A 3270 3250 T C C A A C C A A A A C T A T G G T A G A T A G C T T T G G 3290 3300
FIG.11N	TTTT AAGT	G G T G	T G C (

•		APPROVED G F G F G F G F G F G F G F G F G F G F F
		BY CLASS SUBCLASS
		GRAFISMAN
FIG.11.0	0.1	
CGT	CGTGAAACGCCACGAGGCAGTTCAGGG 3320	•
	GCTATTG	G C A G C A G A G A C T A 3350
GAG(GAGC TGCCAACTATTGGACGGCCG	
		C A A A C G C C C A A T C G 3410
GAGA	GAGATTGAGCA 3430	56

,					4223	Q8 B16B6 M982 FA19 Eagan		
ED E	FIG.12A	Topl alignment	10 20 30 40 50 60 MVOSKONNKSKKSKOVLKLSALSLGLINITQVALANITADKAEA-IDKINLVVVLDETVVT	.Q.QHLFRNILCMTPVYNVQAEQAQEKQTIQ.K .Q.QHLFRNILCMTPAYNVQAGQAQEKQTIQ.K .Q.QHLFRNILCMTPAYNVQAGQAQEKQTIQ.K .TKKPYFRLSIISC.LI.CYVKAESIKDTKE.ISS.VD.QS.E-DSE.ETIS.	70 80 90 100 AKKNA-RKANEVIGLGKVVKTAETINKEQVLNIRDLIRYDP	QKT.RDLSSD.LSQKT.RDLD.LSD	110 120 130 140 150 160 GIAVVEQGRGASSGYSIRGMDKNRVAVLVDGINQAQHYALQGPVAGKNYA-AGGAINEIEYEN	SLTVS.I.S.TA.AALG.TRT.GSS SLTLA.I.S.TA.AALG.TRT.GSS SLTLA.I.S.TA.AALG.TRT.GSS SRLA.I.S.TA.AALG.TRT.GSS

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	4223 Q8 B16B6 M982 FA19 Eagan	•	4223 Q8 B16B6 M982 FA19 Eagan
En E	170 180 190 200 VRSVEISKGANSSEYGSGALSGSVAFVTKTADDIIKDG	220 230 240 250 260 YASKNINAWNISVAAAGKAGSFSGLIIYTDRRQQEYKAHDDAYQGSQSFDRAVA SG.DH.LTQ.L.L.RS.GAEA.LKR.IHKGK.VN.L.L SG.RGLTQ.I.L.RI.GAEA.L.H.G.AG.IRE.GR.VN.L.P SG.RGLTQ.I.L.RI.GAEA.L.H.G.HAG.IREA.GR.VN.LAP SG.RGLTQ.I.L.RI.GAEA.L.H.G.HAG.IREA.GR.VN.LAP	270 280 300 TTDPNINRTFLIANECANENYEACAAGGQTKLQAKPTNPK

SUBSTITUTE SHEET (RULE 26)

FIG. 12C 310 320 330 340 350 360 WRKNNWEDYTGENELIENPLIQDSKSILLERGYQINDK-HYVGGVYEITKQNYANDKTVPR E.KT.STD S. LA. EYG.Q.W.F. WH. DNRA.L.R.Q. TFDIR.M. E.QT.STR K.QT.STR K.QT.STR K.QT.STR K.WYE.Q.WF. G. HFSED I. IF. P.Q. KFDIR.M. SSET.S.S. A. IKMKYE.Q.WF. G. HFSED I. IF. P.Q. KFDIR.M.F. 370 380 YLIVHDIEKSRLSN-HADA. SPIERRDDSSRSFYFM 410 420 440 450 K.KAVFDANKQAGSLR F.KAVFDANKQAGSLR F.KAVFDANKGAGSLR F.KAVFDANKQAGSLR F.KAVFDANKQAGSLR F.KAVFDANKGAGSLR F.KAVF

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FIG. 12D	470 480 490 500 STYPHIDKNCTPDVANKPFSVKEVDANAYKEQHNLIKAVFNHDGSRGY.FYKS.RMI.E.SRFQK .ADGSY.R.SADYYKS.RVI.G.S.R.LQ.A.K .ADGSY.R.SADYYKS.RVI.G.S.R.LQ.A.K .LO.A.K	510 520 530 540 550 560

CLASS SUBCLASS		4223 Q8 B16B6 M982 FA19 Eagan
APPROVED O.G. FIG. BY CLASS SUBI		690 700 A-TWKDDKCKYSETNS-YTNTSPI.RFGNTGNTRQI.LFGNTGNTRQI.LFGNTYFAGQDHN.QGSS.N.
FIG.12E	610 620 630 640 650 660 QKTINTDKI DYQALI DQYDKQNPNSTLKPFEKI KQSLGQEKYNKI DELGFKAYKDLRNEMAGMT	ADCSTTRH: SGNYFIALKUNYTINKYVDIGLGARYDRIKHKSDVPLVINSASNQLSMVFGVV T P. N. G. NG. YA. VQ. VRLGRWA. V. A. I. YRSTH: EDKS. STGTHRN A. I. T P. S. N. KS. YA. VR. VRLGRWA. V. A. I. YRSTH: DGS. STGTHRY A. I. T P. S. N. KS. YA. VR. VRLGRWA. V. A. I. YRSTH: DGS. STGTHRY A. I. T P. S. N. KS. YA. VR. VRLGRWA. V. A. I. YRSTH: DGS. STGTHRY A. I. T P. S. N. KS. YA. VR. VRLGRWA. V. A. I. YRSTH: DGS. STGTHRY A. I. T P. S. N. KS. YA. VR. VRLGRWA. V. A. I. YRSTH: DGS. STGTHRY A. I. T P. S. N. KS. YA. VR. VRLGRWA. V. A. I. YRSTH: DGS. STGTHRY A. I. R KV. L. K. K. YF. ARN. ALG I. VSRT. ANESTI SVGKFRNF T. I.

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APPROVED O.G. FIG. 10 C. C. ASS SUBBARTSHAN BRAFTSHAN	FIG.12F	770 780 800 VKPTNWLDLAYRSSQGFRMPSFSEMYGERFGVT1GKG		YVG.FT.RF.LA.KGDF.NI.I.H.S.A.RNAFALS 870 880 890 900 TLTQGDNAGKQRGKGDLGFHNGQDADLTGINILGRLD R	

O.G. FIG. class subclass				Q8 B16B6 M982 FA19 Eagan		
APPROVED O.G. F.IG. BY CLASS SUBC			970 980 990 1000 NAIFTHSDAKNPSELLADKNLGNGNIQ-TKQATKAKSTP	TM. Y.K. SVD. GSQA.L. ANAK.A-ASRRTR. GML.Y.K. EIT. GSRA.L. SRN. A-ARRTR. GML.Y.K. EIT. GSRA.L. SRN. A-ARRTR. TM. Q.K. SQN. GKRA SRDV.S-RKLIRA		TFS* 08 TFS* B16B6 TFS* FA19 T.T* Eagan
	910 920 930 940 950 960 INAVNSRI,PYGLYSTLAYNKVDVKGKTI,NPTLAG-TNII.FDAIQPSRYVVGLGYDAPSQKWGA	WHG.WGG.DRIK.DADIRADRIFV.SY.V.L.H.DGI.I WNG.WDK.E.W.F.R.H.RDIKKRADRITDIQSH.Q.EG.V WNG.WDK.E.W.F.R.H.RDIKKRADRITDIQSH.S.Q.EG.V F.GLWK.I.W.A.F.Q.K.DQKI.AG.SVSSY.II.H.NT.I	970 NAIFTHSDAKNPSELLADK	TM. Y.K. SVD. GSÇ. GML.Y.K. EIT. GSF. GML.Y.K. EIT. GSF. TM. Q.K. SQN. GKF.	1010 1020 1030 1040 1050 1060 1070 WQTL.DL.SGYVNIKDNFTILRAGVYNVFNITYYTTIWEAL.RQTAEGAVNQHTGL.SQDKHYGRYAAPGRNYQLAL.EMKF*	KNVGV.N. KNVGV.N. KNVGV.N.
	930 940 SKITANPILAG-TNILFDAL(DADIRADRIFV. SYV DIKKRADRIDIQSH DIKKRADRIDIQSH			1030 1040 JENIYYTTWEALRQTAEGAN	L. YR. V
·	910 920 RLPYGLYSTLAYNKVDVKQ	WHG.WGG.DRIK.DADIRADRIFV.SY.WNG.WDK.E.W.F.R.H.RDIKKRADRIDIQSH.WNG.WDK.E.W.F.R.H.RDIKKRADRIDIQSH.F.GLWK.I.W.A.F.Q.K.DQKI.AG.SVSSY.			1010 SGYVNIKDNFTIRAGVYNV	YVT. V. Y. KHL
FIG. 19G	S INAVNSRI	WHG.WGG.WDK.WNG.WDK.			1(MQTT_DLSC	YVT.V YIV.V YIV.V HIV.

4223 Q8 B16B6 M982 FA19 Eagan

PCT/CA97/00163

0.G. FIG.	CLASS SUBCLASS		
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Top2 comparison

	NIGGTNSGIGSANIPEPKYQDVPTEKNEKDK-VSSIQEPAM .AGGAASKDE.K.AEGFDLDSVEVQDMISKEDEKS-QP.SQQD.ENSGAFDLDSVDEAPRPASSPQAQ.DQG -FDLDSVDEAPRPAPSK.P.AR.DQG -FDLDSVDEAPRPAPSK.P.AR.DQG
60 NT-ANAG KANSG	ANTPEPK S MHSK PRPA PRPA
50 ICAVICANAGGIDNIT AAGGAN	70 .GGAA DSVEVQI DSVDEAL
40 NASGSGNTGN GNA	NTGG .A -FDLI -FDLI -FDLI
MCHIPLITICVAISAV-LLITACGGS-GGSNPPAPTPIPNASGSGNTGNTGNGGTIDNT-ANAG NN VNDAAMVLP.F. S. L.G	
20 -LLTACGGS-GG9 SL.G 7SL.G	
THIPLTTICVAISAV-LLTACGGS-GGSNP NNVNQAAMVLP.FSL.G NNVNQAAMVLP.FSL.G NNVNQAAMVLP.FSL.G SVISGGLSFSS	
MKHIPLTT	

...F.M-RIKRR.WHPSANPK.DEVK.KND.WEATGLPTEP.K-..LKQQS.ISEVETN.N-S ..F.M-RIKRR.WYP--GAE.SEVK.NES.WEATGLPTKP.E-..KRQKS.I.KVET..D-S ..VE.-.IRNWIP.EQEEH-A.IN-.N--.VV.LEGDL-.HN.FDN.IWQNIK.SKEVQTVY ----SY..S.STI.KDVK.NNK-...F.V-.LPRR.AHFN.KYK..HKP.GSM.W------..-LQRGEPNSFS.RDE.E---.G. .K. VAQ. .RGNKEPSFIN. DDY.

GYGMALSK INLHNRODTPLD-ERNI I'TL--DGKKQVAEG-KKSPLPFS-LDV-ENKJLDGYTA

PCT	/CA	97/	በበ1	63	

4223 Q8 B16B6 M982 FA19 FA19 G8 B16B6 M982 FA19	Eagan
FIG. 13B 150 170 180 190 200 200	. TN VNGVATI.ATKGK.YPLLSNG.H

APPROVED O.G. FIG.	· · ·		TSK-HPFTSDAN 4223 KK Q8 .NGSISD B16B6 ET.LV.SS M982 GT.LVF.SS FA19 SEEEGT Eagan	
	FIG.13C	GMYYGASSKD-EYNRLLTKEDSAPDGHSGEYGHSSEFTVNFKEKKLTGKLFSNLQDRHKGN .DR.S.M. YHPSD.KNKNYND.SK.S.K.E.SIGS DK-SL.ALEGV.RNQAE-ASSTD-F.MTE.D.SD.TIK.T.YR.NRIT.NNSENK DR.S.F.GDGS.EYSNKNSTLK.D.EFT.NLE.D.GNIR.NAS.NNNTNND DK.S.F.GDGS.TTSNRDSNLN.K.EFT.N.K.D.NNIR.NKVINTAASDGRRAIP.DID.EN-DSKNGILISADGGTQYTKRKTNNQPYE 370 380 400	VIKTERYDIDANIHGNRFRGSATASNKNDTSK-HPFTSDAN N.KYDTTEASKK QITT.Q.TLK.K.L.ADGA.NGSISD KHT.QY.SLQ.TN.TTD.K-ENET.LVSS YY.SLTLRS.K.I.TD.PNTGGT.LVF.SS KK.LD.YSTVKPTESEEEGT	410 420 430 440 NRLEGGFYGPKGEEL AGKFLTNDNKLFGVFGAKRESKAEEKTES

		67/90	
ASS	4223 Q8 B16B6 M982 FA19 Eagan	•	4223 Q8 B16B6 M982 FA19 Eagan
THE	450 460 470 480AILDAYALGTFNTSNATTFTPFTEKQLDNFGNAKKLVTVIRITGEEFKKE.I.SDVL NSKLTTVVE.TLNDKKI.NSAQ ETRLTTVVE.TPDGKEI.NSTR KTNATTSTA.NITTDTTANTI.DEKN.KTEDISSE.DY.L	510 520	

09/142628

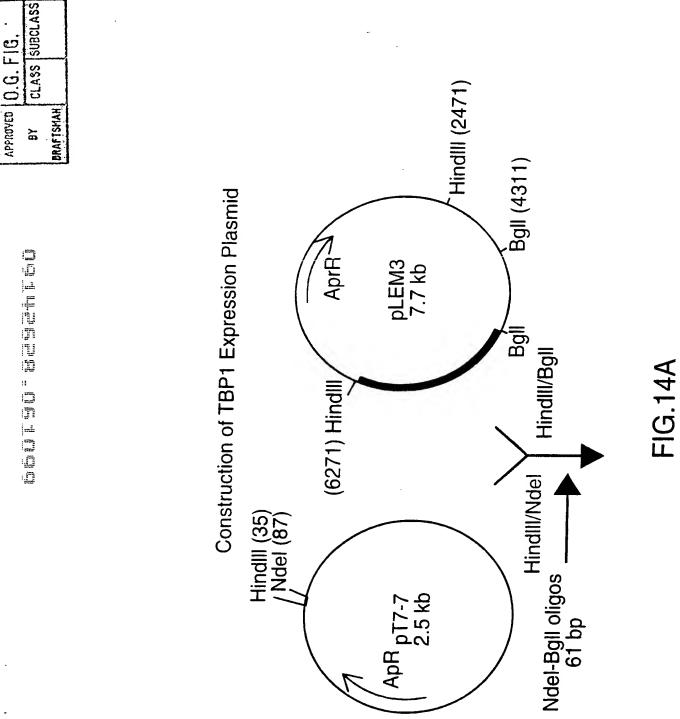
	TO THE
FIG. 13E	3E
	550 570 SVFLQGERTATIGEKAVPTIGTAKYI.G
SAMQAGG- SVMQAVK- KETETETIE	SAMQAGGNSSQADAKTEQVEQ.MD.NKI.QEQGIV SVMQAVKNSSQADAKTKQIEQ.MD.NKI.QEQGIV KETETETETETETEKDKEKEKEKEKEKQTAATTNTYYOL.HPKDDI K.S.H
	600 610 DAQDVADFTIDFGNKSVSGK
	T.YANTSWS.EANQEGGNR.E.DVST.KIT B16B6 S.Y.H.ANTSWS.NADKEGGNR.EVN.AD.KIT M982 F.Y.R.ANTSWS.KANATDGNR.KVN.DR.EIT.T FA19 S.YDTSYSPS.DKKR.KNA.E.NV.AF.KIT.F
LITKGRQD T.Q TA.D.TS TAEN.A TAEN.SE	

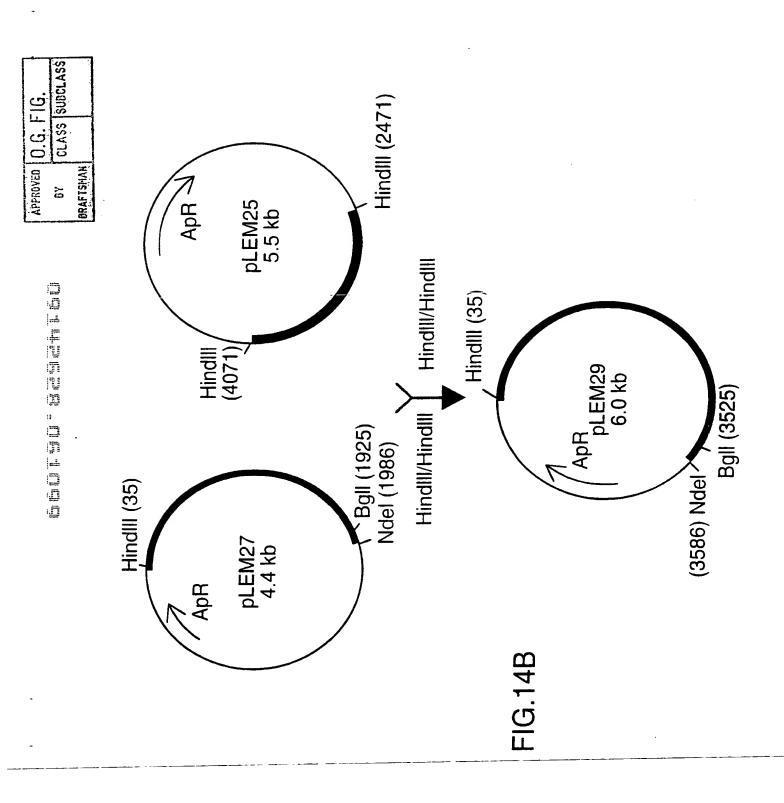
	1.0	_
	SUBCLASS	_
0.6. FIG.	CLASS	
APPROVED O.G. F. G.	, 6 7	

4223	4223
Q8	Q8
B16B6	B16B6
M982	M982
FA19	FA19
Eagan	Eagan
680 PNANEMGSFTNADDSKASV K.ISFPGNAPEGKQEHDT. K.E.L.W.AYPGDKQTEKATATSSDGSAST. E.L.W.AYPGNEQIKNAIVESGNGSAST. K.S.L.Y.YNGNSTAINSESSSTVSSS.SKNAP.A.	

FIG. 13F

700
VFGTKRQQEV-K*
....E..-.*
...A...L.Q-*
...A...P.Q-*
...A...KL.-.*





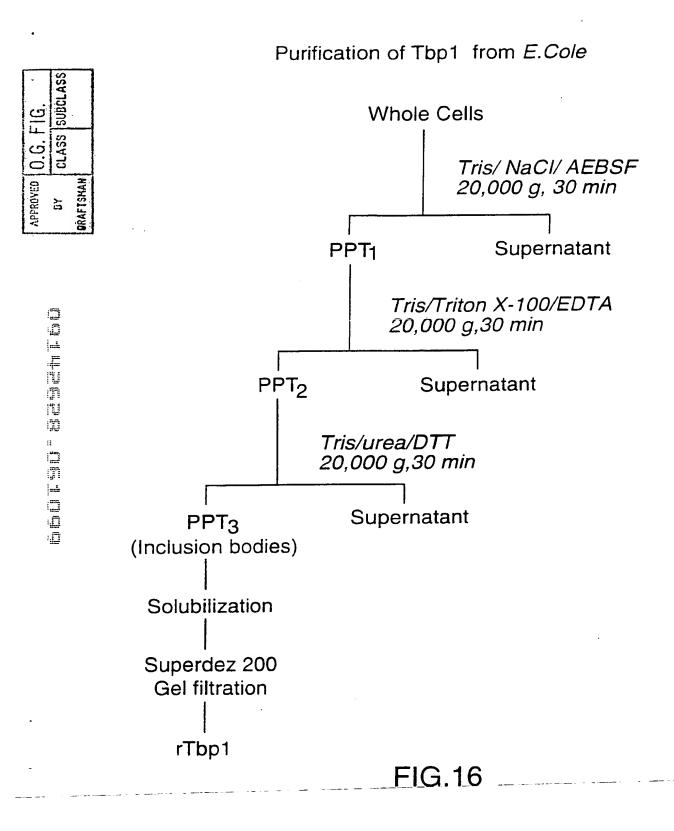
Expression of rTbp1 in E. coli

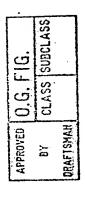
0.G. FIG.	CLASS SUBCLASS	
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Molecular Weight (x 10 ⁻³)	205 - 117 - 80 - 50 - 33 - 28 - 19 -	The second secon				← Tbp1
		1	2	3	4	

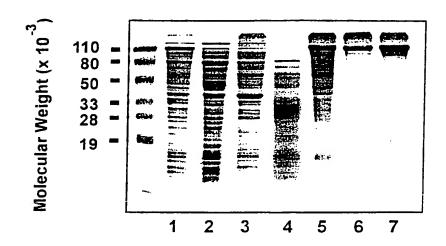
- 1. Prestained molecular weight markers
- 2. pLEM29B-1 lysate, non-induced
- 3. pLEM29B-1 lysate, 1 hr post-induction
- 4. pLEM29B-1 lysate, 3 hr post-induction

Fig.15

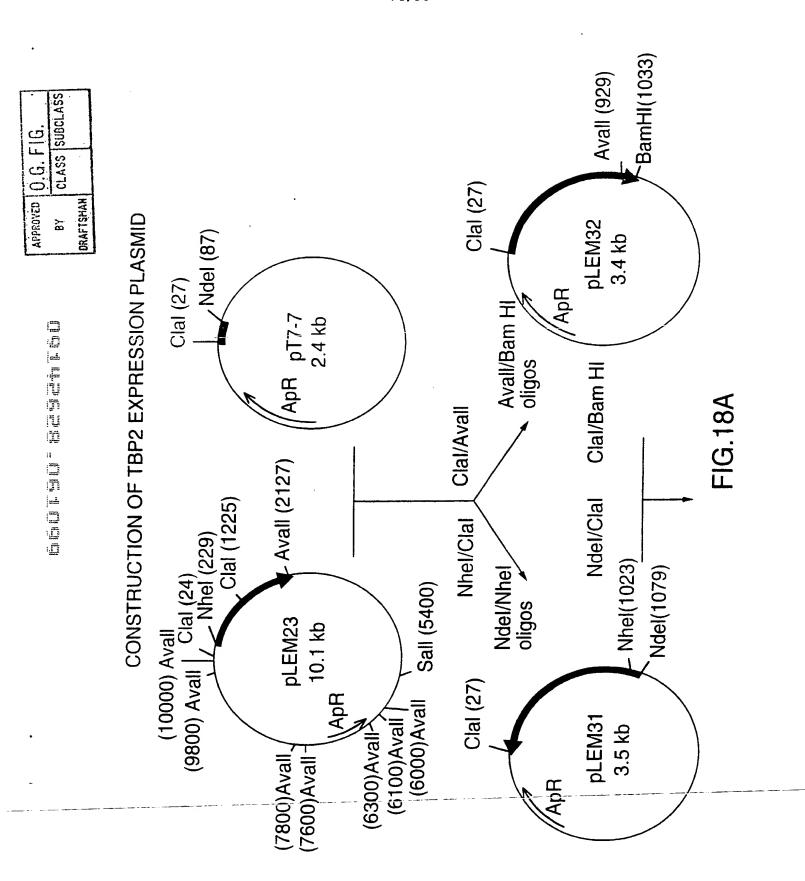




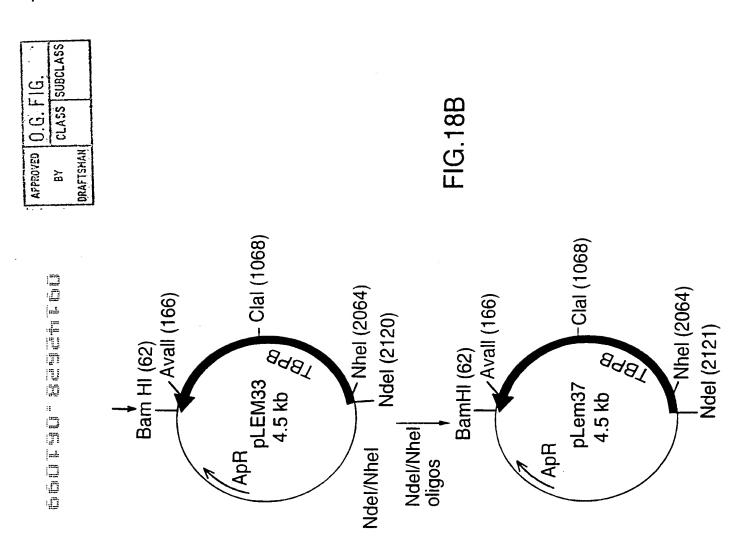
Purification of rTbp1 from E. coli



- 1. E. coli Whole cells
- 2. Soluble proteins after 50 mM Tris/ NaCl extraction
- 3. Soluble proteins after Tris/ Triton X-100/ EDTA extraction
- 4. Soluble proteins after Tris/ urea/ DTT extraction
- 5. Left-over pellet (rTbp1 inclusion bodies)
- 6.7. Purified rTbp1



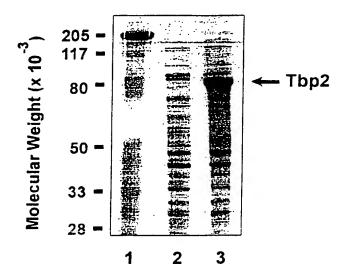
PCT/CA97/00163



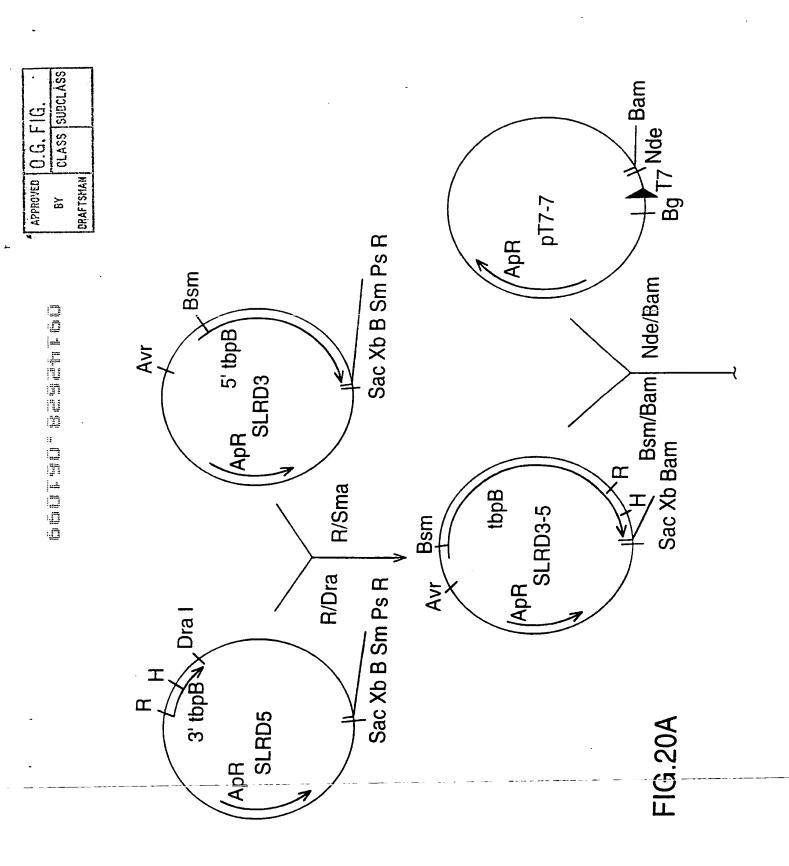
оуер O.G. FIG.

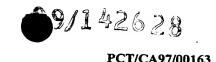
Y CLASS SUBCLASS

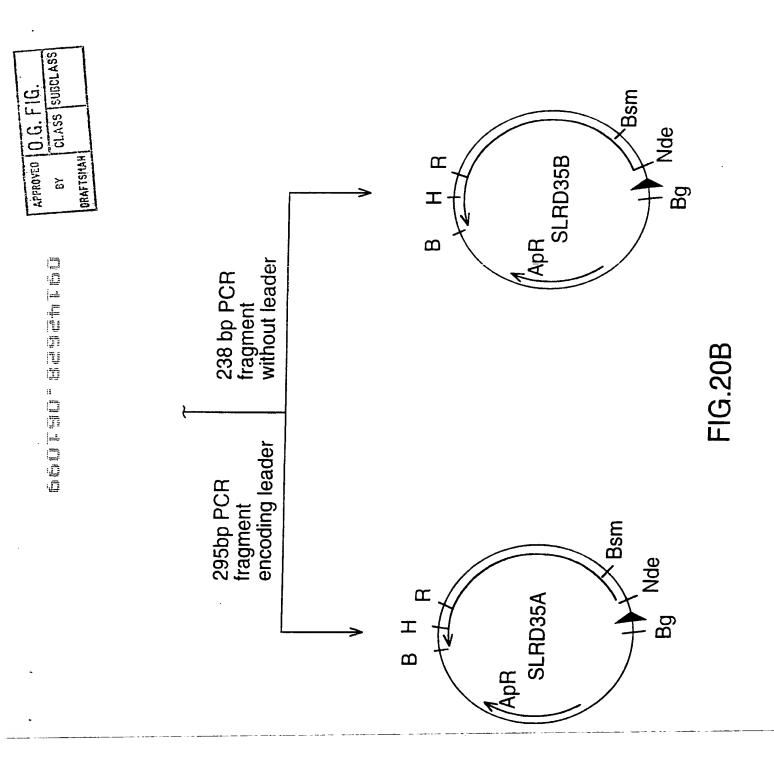
Expression of rTbp2 in E. coli



- 1. Prestained molecular weight markers
- 2. pLEM37B-2 lysate, non-induced
- 3. pLEM37B-2 lysate, induced

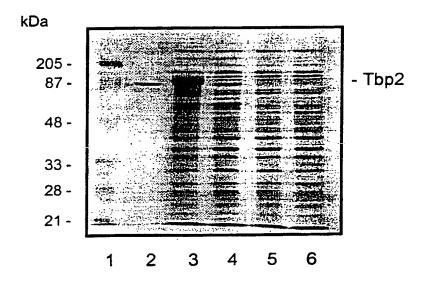






DOTHERM RETURN

Fig 21. Expression of Q8 rTbp2 protein in E. coli



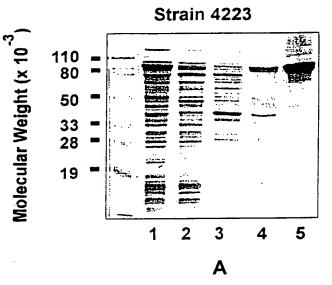
- Prestained molecular weight markers
- 4223 rTbp2 protein
- SLRD35A lysate, 3 hr post-induction
- SLRD35B lysate, 3 hr post-induction
- SLRD35A lysate, non-induced
- SLRD35B lysate, non-induced

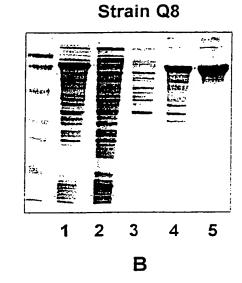
rTbp2

FIG.22

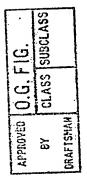


Purification of rTbp2 from E. coli

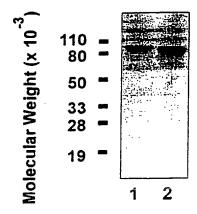




- 1. E. coli Whole cells
- 2. Soluble proteins after 50 mM Tris extraction
- 3. Soluble proteins after Tris/ Triton X-100/ EDTA extraction
- 4. Left-over pellet (rTbp2 inclusion bodies)
- 5. Purified rTbp2



Binding of Tbp2 to Human Transferrin



- 1. rTbp2 (strain 4223)
- 2. rTbp2 (strain Q8)

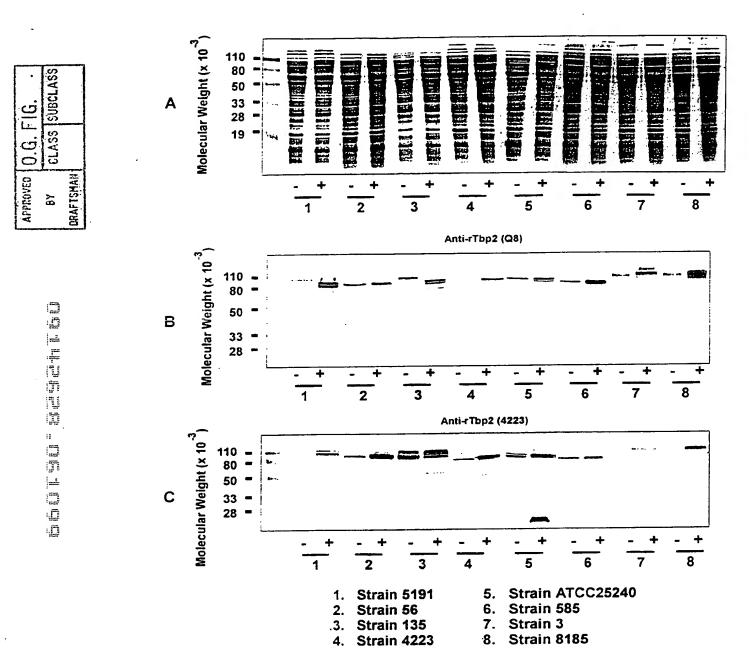


Fig.25

Figure 26 Restriction map of M. catarrhalis strain R1 tbpB

1		537	1073	1609	2145
enzyme		ļ			
Alwni _					
AseI					
Asnī					
Bani		·			<u></u>
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BepMI	1 ! !			· · · · · · · · · · · · · · · · · · ·	 ¦
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DdeI			:	1	
DraI				·	
EcoRI				!	
ECORV			:		
FokI	!				:
HinfI					
MaeI	_!		11		
MaeII	1				
Mali !		· · · · · · · · · · · · · · · · · · ·			
Ncol	!	·			
NneI	_ :				
Real					!
Sep I					!
Styl	!				
TaqI		·!			!
Tth1111			 		_:!
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APPROVED O.G. FIG.

BY CLASS SUBCLASS
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Figure 77 Nucleotide and deduced amino acid sequence of M. catarrhalis R1 tbpB

TGT	CAGO	ATGC	CAAA	ATAG	GCAT	TAAC	AGAC	TTT	TTAG	AATA	TACC	LATCA	LACCO	ATC	GAGG	ATTA	TTTT
								27									54
ATG	AAA	CAC	ATT	CCI	TTA	ACC	ACA			GTG	GCA	ATC	: TCI	GCC	GTC	TTA	TTA
																	Leu
	-	mcm.			N.C.T.	com	com	81			000			3.00			108
													CCT Pro				
1111	ALG	Cys	GIY	G_y	261	Gry	Giy	361	ASII	110	720	ALG	PLO	1111	FIQ	1-6	PIO
								135									162
													GCT				
Asn	Ala	Ser	Gly	Ser	Gly	Asn	Thr	Gly	Asn	Thr	Gly	Asn	Ala	Gly	Gly	Thr	Asp
								189									216
TAA	ACA	GCC	AAT	GCA	GGT	AAT	ACA		GGT	ACA	AGC	TCT	GGT	ACA	GGC	AGT	
													Gly				
								243									270
													CCC				
Ser	1112	267	Gin	FIO	гууь	ıyı	لننى	Asp	VAI	PLO	11.1	1,111	Pro	Abii	ASII	Lys	GIU
•								297									324
CAA	GIT	TCA	TCC	ATT	CAA	GAA	CCT	GCC	ATG	GGT	TAT	GGC	ATG	GCT	TTG	AGT	AAA
Gln	Val	Ser	Ser	Ile	Gln	Glu	Prc	Ala	MET	Gly	Tyr	Gly	MET	Ala	Leu	Ser	Lys
								251									370
ATT	ידגג	מייי	TAC	GAC	CAA	ממה	GAC	351 ACG	CCA	7 *⊤"∆	GAT	GCA	AAA	דבב	ATC	ייידא	378 acc
													Lys				
			-	-			-				-		-				
								405									432
													CCA				
Deu	Asp	сту	-y	гЪз	G111	Val	AId	Asp	ASII	GIII	Lys	ser	Pro	THE	PIO	File	Ser
								459									486
TTA	GAT	GTA	GAA	AAT	AAA	TTG	CTT	GAT	GGC	TAT	ATA	GCA	AAA	ATG	AAT	GAA	GCG
Leu	Asp	Val	Glu	Asn	Lys	Leu	Leu	Asp	Gly	Tyr	Ile	Ala	Lys	MET	Asn	Glu	Ala
								F43									-40
GAT	444	דעע	GCC	ناست⊽	CCT	445)	ACA	513 ETT	מאמ	A:0.4	CAA	דעע	GAA	ממה	<u>አ</u> ልጥ	444	540
													Glu				
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								567									594
ATA																	
TIE	ser	Asp	en	GIN	тел	ATS	туу	ηλε	ı-e	гÀг	GIU	ASR	Val	ATG	-yya	ser	PIO
								621									648
GAG	TTT	CAG	CAA	GTA	TTA	TCA			AAA	GCG	AAA	ACT	TTC	CAT	TCA .		
03	Db -	~ 3	63 -		•	C	0	- 3 -	-	3.1 -	T	773	Dha-		F)	>	.

Giu Phe Gin Gin Val Leu Ser Ser Ile Lys Ala Lys Thr-Phe-His Ser Asn Asp

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•										67	5								702
S	7	AA	A AC	A AC	CAA	A GCZ	A ACC	ACA	A CG	A GA	T TI	AA A'	A TA	r gr	T GA	T T	ri Go	T T	AC TAC
1G. suaclass	1	цу	S _11	r in	т. гъ	S Alt	i Thr	Thi	Arg	g As	p Le	u Ly	s Ty	r Va	l As	pΤ	r Gl	.у Т _}	Tyr
	1									77	_								
128		TT	GGT	G AA	T GA	r gar	יים ב	י מידי	י רידי	72 2 2 2		C 33	N NC:						756 T TGG
33	1	Lei	u Va	l As	n Asi	Ala	Asn	Tvr	Ten	i Th	r Va	L AA	A ALA	A GA	- AA	G CC	A AA	A CI	T TGG u Trp
O.G.											L Va.	r ny	B 1111	ASI) As	n Pr	о гу	's Le	u Trp
										783	3								
8	₹	AA	r TC	A GG	r cci	GTG	GGC	GGT	GIG	TT	TAT	r aa:	r GGC	TCZ	AC	G AC	ר פר	~ AA	810 A GAG
24 25 26 26 26 26 26 26 26 26 26 26 26 26 26	2	Asr	ı Sei	r Gly	y Pro	Val	Gly	Gly	Val	Phe	Ty:	c Ası	Gly	Ser	Th	Th	r Al	a iv	s Glu
8	ORAFTSHAN												-					,	010
	9-1									837	7								864
•		CIC	3 CCC	ACA	A CAA	GAT	GCG	GTC	AAA	TA!	' AA	A GGA	CAT	TGG	GAC	TT	r Atc	G AC	CGAT
		Let	Pro	e Tinz	r GIII	Asp	Ala	Val	Lys	Тут	Lys	Gly	His	Trp	Asr	Phe	ME:	r Thi	C Asp
										901									
		GTT	· GCC	' AAA	444	ZCZ	ממ	CGA	بلمليك	891		CTA	2.23	~~~	3.00				918 A GG C
		Val	Ala	Lvs	Lvs	Arg	Asn	Ara	Phe	Ser	GAM	Val	AAA Taro	GAA	ACC	TA	CA	A GCZ	A GGC A Gly
12				-	-3-	3		5		201	010	Val	ny a	GIU	1111	171	GII	1 Alé	Gly
1										945									972
s.L		TGG	TGG	TAT	GGG	GCA	TCT	TCA	AAA	GAT	GAA	TAC	AAC	CGC	TTA	TTA	ACC	מממ :	CCE
<u>_</u>		Irp	Trp	Tyr	Gly	Ala	Ser	Ser	Lys	Asp	Glu	Tyr	Asn	Arg	Leu	Leu	Thr	Lvs	Ala
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Ī		C > m	-							999			,						1026
IJ		ga1	215	SCA.	CCT	GAT	AAT	TAT	AGC	GGT	GAA	TAT	GGT	CAT	AGC	AGT	GAA	TIT	ACT
Ä		raħ	ALG	WIG	Pro	wab	ASII	ıyı	ser	GIY	GIU	Tyr	Gly	His	Ser	Ser	Glu	Phe	Thr
:1									٦	053									
		GTT	AAT	TTT	AAG	GAA	AAA	ΑΑΛ			CCT	GAG	C	ملكلهمة	8 /Tr	220			1080
177		Val	Asn	Phe	Lys	Glu	Lvs	Lvs	Leu	Thr	Glv	Glu	Len	Dhe	Cor	Ann	LON	CAA	GAC
, mil					-		•				- 1				261	woll	Leu	GIII	Asp
132										107									1134
·E		AGC	CAT	AAA	CAA	AAA	GTA 2	ACC .	AAA	ACA	AAA	CGC	TAT	GAT	ATT	AAG	GCT	GAT	ATC
·D		Ser	His	Lys	Gln	Lys	Val '	Thr :	Lys	Thr	ľàs	Arg	Tyr	qeA	Ile	Lys	Ala	Asp	Ile
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		ראר	acc	አአ ር	000	. Care		700	1	161								3	1188
		Fis	Glv	AAK.	CGC	Dpo	CGI. (3GC 1	AGT	GCC	ACC	GCA	AGC	GAT .	AAG	GCA	GAA	GAC	AGC
		******	CTY	A3.1	Arg	FILE A	ary (эту з	ser .	AIa	Thr	Ala	Ser .	qzA	Lys	Ala	Glu	Asp	Ser
									7	215									240
		AAA	AGC	AAA	CAC	ccc :	TTT Z	ACC A			GCC	מממ	ርልጥ	. מממ	~~~	C 2 2	dam		242
		Lys	Ser	Lys	His	Pro !	Phe 1	Chr S	Ser 2	Asp	Ala	Lvs	Asp 1	Lve	ien Ien	Gl	G112	GD-	Dan
				-						F		, ~		-y	u		GTÅ	a1 Å	FILE
									13	269								-	296
		TAT	GGA	CCA	AAA	GGC (BAG G	AG C	TG (GCA ·	GGT .	AAA	TTC :	TA I	ACC	GAT	GAT	AAC	AAA
		Tyr	Gly	Pro	Lys (Gly G	Slu C	lu I	eu i	Ala	Glv	Lvs	Phe 1	et!	Th∽	Agn	Aun	yen	Lago

Tyr Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Thr Asp Asp Asn Lys

CTC TTT GGT GTC TTT GGT GCC AAA CAA GAG GGT AAT GTA GAA AAA ACC GAA GCC Leu Phe Gly Val Phe Gly Ala Lys Gln Glu Gly Asn Val Glu Lys Thr Glu Ala

	137	7	1404
ATC TTA GAT GCT TA	T GCA CTT GGG AC	A TTT AAT AAA CCT	GGT ACG ACC AAT CCC
Ile Leu Asp Ala Ty	r Ala Leu Gly Thi	Phe Asn Lys Pro	Gly Thr Thr Asn Pro

1431 1458 GCC TTT ACC GCT AAC AGC AAA AAA GAA CTG GAT AAC TTT GGC AAT GCC AAA AAG Ala Phe Thr Ala Asn Ser Lys Lys Glu Leu Asp Asn Phe Gly Asn Ala Lys Lys

TTG GTC TTG GGT TCT ACC GTC ATT GAT TTG GTG CCT ACT GAT GCC ACC AAA GAT Leu Val Leu Gly Ser Thr Val Ile Asp Leu Val Pro Thr Asp Ala Thr Lys Asp

1539 1566 GTC AAT GAA TTC AAA GAA AAG CCA AAG TCT GCC ACA AAC AAA GCG GGC GAA ACT Val Asn Glu Phe Lys Glu Lys Fro Lys Ser Ala Thr Asn Lys Ala Gly Glu Thr

TTG ATG GTG AAT GAT GAA GTT AGC GTC AAA ACC TAT GGC AAA AAC TTT GAA TAC Leu MET Val Asn Asp Glu Val Ser Val Lys Thr Tyr Gly Lys Asn Phe Glu Tyr

CTA AAA TIT GGT GAG CTT AGT GTC GGT AGC CAT AGC GTC TIT TTA CAA GGC Leu Lys Phe Gly Glu Leu Ser Val Gly Gly Ser His Ser Val Phe Leu Gln Gly

1701 1728
GAA CGC ACC GCT ACC ACA GGC GAG AAA GCC GTA CCA ACC ACA GGC AAA GCC AAA
Glu Arg Thr Ala Thr Thr Gly Glu Lys Ala Val Pro Thr Thr Gly Lys Ala Lys

1755 1782
TAT TTG GGG AAC TGG GTA GGA TAT ATC ACA GGA GCG GAC TCA TCA AAA GGC TCT
Tyr Leu Gly Asn Trp Val Gly Tyr Ile Thr Gly Ala Asp Ser Ser Lys Gly Ser

1836
ACC GAT GGC AAA GGC TTT ACC GAT GCC AAA GAT ATT GCT GAT TTT GAC ATT GAC
Thr Asp Gly Lys Gly Phe Thr Asp Ala Lys Asp Ile Ala Asp Phe Asp Ile Asp

1863 1890
TTT GAG AAA AAA TCA GTT AAT GGC AAA CTG ACC ACC AAA GAC CGC CAA GAC CCT
Phe Glu Lys Lys Ser Val Asn Gly Lys Leu Thr Thr Lys Asp Arg Gln Asp Pro

1917 1944 GTC TTT ÄAC ATC ACA GGT GAA ATC GCA GGC AAT GGC TGG ACA GGT AAA GCC AGC Val Phe Asn Ile Thr Gly Glu Ile Ala Gly Asn Gly Trp Thr Gly Lys Ala Ser

 $1971 \\ ACC GCC GAA GCG AAC GCA GGG GGC TAT AAG ATA GAT TCT AGC AGT ACA GGC AAA Thr Ala Glu Ala Asn Ala Gly Gly Tyr Lys Ile Asp Ser Ser Thr Gly Lys$

2052
TCC ATC GTC ATC AAA GAT GCC GTG GTT ACA GGT GGC TTT TAT GGT CCA AAT GCA
Ser Ile Val Ile Lys Asp Ala Val Val Thr Gly Gly Phe Tyr Gly Pro Asn Ala

WO 97/32980

89/90

F4 27 (cars)

2079

2106

PCT/CA97/00163

ACC GAG ATG GGT GGG TCA TTT ACA CAC AAC AGC GGT AAT GAT GGT AAA GTC TCT Thr Glu MET Gly Gly Ser Phe Thr His Asn Ser Gly Asn Asp Gly Lys Val Ser

2133

GTG GTC TTT GGC ACA AAA AAA CAA GAA GTT AAG AAG TGA Val Val Phe Gly Thr Lys Lys Gln Glu Val Lys Lys *

APPROVED O.G. F

BY CLASS

DRAFTSMAH

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u	70	

PCT/CA97/00163

				90.	/90		
-	4223 Q8 R1	4223 Q8 R1	4223 Q8 R1	4223 Q8 R1	4223 Q8 R1	4223 Q8 R1	4223 Q8 R1
Fig. 28 Fig. 28 APPROVED O.G. FIG. " By CLASS SUBCLASS Aliqument of M. catarrhalls Tbp2	MKHIPLITICVAISAVLLTACGGSGGS-NPPAPTPIPNASGSGNTGNTGNAGGTDNTAN-AGNTGGTNSGTGSANTPEPKYQDVPTEKNEKDKVSSIQEFAM SGGANSGAGGANSGASTP.N.EQTP.N.EQ	GYGMAL,SKINLHURQDTPLDEKNIITLDGKKQVAEGKKSPLPFSLDVENKLLDGYIAKONVADKNAIGDRIKKGNKEISDERLAKQIK-BAVRKSHBFQQVVB. ICLR.WIPQRQEEHAKI TNDVVKLEGDLKHNPFDNSIWQNIK.SKEVQTVYNQEKQNIEDQIK.EN.QRPDKKLDDV.L.AYI.K.LDDRLTELAXDQADNQP	LSSLENKIFHSNDGTTKATTRDLKYVDYGYYLANDGNYLTVKTDKLWNLGPVGGVFYNGTTTAKELPTVDAVKYKGHWDFMTDVANRRNRFSBVKENSQA KPIY.KN.NY.H.KQN.RRS.IYRSGYSNIIPIAKT.FD.AL.Q.Q.Q.VSQTAKKGQSFS.FGTSQRL.	310 370 380 400 GWYYGASSKDBYNRLLTKEDSAPDGHSGRYGHSSBFTVNFKEKKLTGKLFSNLQDRHKGNVTKTERYDIDANIHGNRPRGSATASNKNDTSKHPFTSDAN DR.S.M. YH. PSD. KNKNYND.SK.S.K.E.SIGS.NKYDTTEASK	#10	S10	610 620 630 640 650 660 570 680 690 700 DFGNKSVSGKLITKGRQDPVFSITGQIAGNGWTGTASTTKADAGGYKIDSSSTGKSIAIKDANVTGGFYGPNANEMGGSFTHNA-DDSKASVVFGTKRQQLVK-*
A IA	X ::	S. :	ST :	GW.	NRI S. DK.	DKE B	070 B